

GenCore version 5.1.6
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | Score | Query Match Length | DB ID | Description | |
|------------|-------|--------------------|-------|--------------------|--------------------|
| 1 | 298 | 100.0 | 585 | Sequence 805, App | |
| 2 | 249 | 83.6 | 641 | Sequence 12391, A | |
| 3 | 249 | 83.6 | 623 | Sequence 1614, A | |
| 4 | 249 | 83.6 | 880 | Sequence 11768, A | |
| 5 | 249 | 83.6 | 1039 | Sequence 17348, A | |
| 6 | 249 | 83.6 | 1663 | Sequence 1531, A | |
| 7 | 249 | 83.6 | 1663 | Sequence 1621, A | |
| 8 | 248 | 83.2 | 680 | Sequence 1613, A | |
| 9 | 248 | 83.2 | 743 | Sequence 1612, A | |
| 10 | 248 | 83.2 | 802 | Sequence 93169, A | |
| 11 | 247 | 82.9 | 666 | Sequence 6714, A | |
| 12 | 247 | 82.9 | 925 | Sequence 10354, A | |
| 13 | 247 | 82.9 | 974 | Sequence 115917, A | |
| c | 14 | 82.9 | 974 | Sequence 1609, A | |
| c | 15 | 244 | 81.9 | 580 | Sequence 74300, A |
| c | 16 | 244 | 81.9 | 1656 | Sequence 1530, A |
| c | 17 | 244 | 81.9 | 1656 | Sequence 1620, A |
| c | 18 | 243 | 81.5 | 669 | Sequence 1686, A |
| c | 19 | 243 | 81.5 | 634 | Sequence 1615, A |
| c | 20 | 243 | 81.5 | 834 | Sequence 90376, A |
| c | 21 | 242 | 81.2 | 961 | Sequence 1204, A |
| c | 22 | 242 | 81.2 | 603 | Sequence 132529, A |
| c | 23 | 242 | 81.2 | 603 | Sequence 77029, A |
| c | 24 | 242 | 81.2 | 825 | Sequence 1529, A |
| c | 25 | 242 | 81.2 | 825 | Sequence 1616, A |
| c | 26 | 242 | 81.2 | 961 | Sequence 5549, A |
| c | 27 | 242 | 81.2 | 999 | Sequence 170166, A |
| c | 28 | 239 | 80.2 | 1215 | Sequence 112793, A |
| c | 29 | 239 | 80.2 | 1235 | Sequence 1608, A |
| c | 30 | 237 | 79.5 | 1120 | Sequence 34431, A |
| c | 31 | 232 | 77.9 | 999 | Sequence 1532, A |
| c | 32 | 232 | 77.9 | 999 | Sequence 1622, A |
| c | 33 | 232 | 77.9 | 1092 | Sequence 1295, A |
| c | 34 | 230 | 77.2 | 748 | Sequence 29, App |
| c | 35 | 230 | 77.2 | 748 | Sequence 1, App |
| c | 36 | 230 | 77.2 | 748 | Sequence 15, App |
| c | 37 | 230 | 77.2 | 748 | Sequence 63, App |
| c | 38 | 230 | 77.2 | 748 | Sequence 85, App |
| c | 39 | 230 | 77.2 | 748 | Sequence 103, App |
| c | 40 | 202 | 67.8 | 577 | Sequence 115975, A |
| c | 41 | 197 | 66.1 | 724 | Sequence 1, App |
| c | 42 | 197 | 66.1 | 724 | Sequence 14, App |
| c | 43 | 197 | 66.1 | 724 | Sequence 18, App |
| c | 44 | 197 | 66.1 | 1306 | Sequence 2611, App |
| c | 45 | 197 | 66.1 | 1306 | Sequence 17, App |

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26: /cgn2_6/podata/1/pubnpn/us60_PUBCOMB.seq:*

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No
is the number of results predicted by chance to have a

; APPLICANT: Jiang, Cai-Zhong
 ; APPLICANT: Sahaha, Raymond R.
 ; APPLICANT: Pilgrim, Marsha L.
 ; APPLICANT: Creelman, Robert A.
 ; APPLICANT: Dubell, Arnold N.
 ; APPLICANT: Ratcliffe, Oliver
 ; APPLICANT: Kumimoto, Roderick K.
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
 ; FILE REFERENCE: MBI-0048CLP
 ; CURRENT FILING DATE: 2003-04-10
 ; PRIORITY NUMBER: US/10/412,699B
 ; PRIORITY NUMBER: 2003-04-10
 ; PRIORITY NUMBER: 09/394,519
 ; PRIORITY NUMBER: 1999-09-13
 ; PRIORITY NUMBER: 09/489,376
 ; PRIORITY NUMBER: 2000-01-21
 ; PRIORITY NUMBER: 09/506,720
 ; PRIORITY NUMBER: 09/506,720
 ; PRIORITY NUMBER: 09/533,010
 ; PRIORITY NUMBER: 2000-03-22
 ; PRIORITY NUMBER: 09/533,392
 ; PRIORITY NUMBER: 2000-03-22
 ; PRIORITY NUMBER: 09/533,029
 ; PRIORITY NUMBER: 09/533,029
 ; PRIORITY NUMBER: 09/532,551
 ; PRIORITY NUMBER: 2000-03-22
 ; PRIORITY NUMBER: 09/533,648
 ; PRIORITY NUMBER: 2000-03-22
 ; PRIORITY NUMBER: 09/713,994
 ; PRIORITY NUMBER: 2000-11-16
 ; PRIORITY NUMBER: 09/819,142
 ; PRIORITY NUMBER: 2001-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PA
 ; NUMBER OF SEQ ID NOS: 2011
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 805
 ; LENGTH: 585
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; OTHER INFORMATION: G1274
 ; US-10-412,699B-805

Alignment Scores:
 Pred. No.: 7.25E-35 Length: 585
 Score: 298.00 Matches: 54
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 18 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-412-699B-805 (1-585)

Qy 1 Asp[Gly]Phelv[Trp]Arg[Leu]GlySerVallethrthrGluGlyValHis 54
 Db 331 GATGGTTTAATGGAGGTAGTCAGAAACTCTGTCAAACAAACATTAAAC

Qy 21 Asn[Tyr]TyrLysCysSerGluGlyCysserVallethrthrGluGlyValHis 54
 Db 391 ARTTACTAGAATGTCATGTGAAAGTTCTCGTGAGCAAGGGTGTGAGCAAG

Qy 41 Asp[Asp]AlaAlaTyrVallethrthrGluGlyValHis 54
 Db 451 GACGTGACGCTTATGTAATTACACATATGAAGGAGTCAT 492

RESULT 2
 US-10-425-114-12391
 ; Sequence 12391, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yindu
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Kovacic, David K.

PRIOR APPLICATION NUMBER: 09/533,030
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/533,392
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/533,029
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/532,591
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/533,648
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/713,994
 PRIOR FILING DATE: 2000-11-16
 PRIOR APPLICATION NUMBER: 09/819,142
 PRIOR FILING DATE: 2001-03-27
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NAME OF SEQ ID NOS: 2011
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 1614
 LENGTH: 823
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (9)..(9)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (802)..(802)
 OTHER INFORMATION: n is a, c, g, or t
 US-10-412-698-1614

Alignment Scores:
 Pred. No.: 2.84e-27 Length: 823
 Score: 249.00 Matches: 44
 Percent Similarity: 88.89% Conservative: 4
 Best Local Similarity: 81.48% Mismatches: 6
 DB: 0 Indels: 0 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-412-698-1614 (1-823)

Qy 1 AspGlyPhenylStpArgLsTyrGlyLysSerVallysAsnAlylAsnLysBrg 20
 Db 441 GACGGATTCAAGTGAAAGTAGCGGAAGAACGGCTCAAGACGCCAAATCCACG 500

Qy 21 AsntrytlycSserserGluGlyCysSerVallysArgVallysGluGly 40
 Db 501 AACTACTACCCTGTCTGGGGCTGGGGCTGGGGCTGAAGAGCGGTGAGGGACCC 560

Qy 41 AspAspAlalaAlaTyrValleThrTyrGluGlyValHis 54
 Db 561 GACGACCCCCCTACCTCATCACCCACTAGACGSGTCAC 602

RESULT 4
 US-10-767-701-11768
 ; Sequence 11768, Application US/10767701
 ; Publication No. US2004012684A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
 ; FILE REFERENCE: 38-21153535JB
 ; CURRENT APPLICATION NUMBER: US/10/767,701
 ; CURRENT FILING DATE: 2004-01-29
 ; SEQ ID NO 11'68
 ; LENGTH: 880
 ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS16930_1
 ; FEATURE: Sorghum bicolor

US-10-767-701-11768
 Alignment Scores:
 Pred. No.: 3.1e-27 Length: 880
 Score: 249.00 Matches: 44
 Percent Similarity: 88.89% Conservative: 4
 Best Local Similarity: 81.48% Mismatches: 6
 DB: 19 Indels: 0 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-767-701-11768 (1-880)

Qy 1 AspGlyPhenylStpArgLysTyrGlyLysSerVallysAsnAlylAsnLysBrg 20
 Db 391 GATGGATTCAAATGGAAAGATGGAGAAGCTGTCAGAACGCCAAATCCACG 450

Qy 21 AsntrytlycSserserGluGlyCysSerVallysArgVallysGluGly 40
 Db 451 AACTACTACCCTGTCTGGGGCTGGGGCTGAAGAGCGGTGAGGGACCC 510

Qy 41 AspAspAlalaAlaTyrValleThrTyrGluGlyValHis 54
 Db 511 GACGACCCCCGTACGTATCACCACTAACGACGGCGTCAC 552

RESULT 5
 US-10-425-115-73408
 ; Sequence 73408, Application US/10425115
 ; Publication No. US2004014272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-211532JB
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO: 73408
 ; LENGTH: 1039
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT1577_166948C.1
 ; US-10-425-115-73408

Alignment Scores:
 Pred. No.: 3.89e-27 Length: 1039
 Score: 249.00 Matches: 44
 Percent Similarity: 88.89% Conservative: 4
 Best Local Similarity: 81.48% Mismatches: 6
 DB: 20 Indels: 0 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-425-115-73408 (1-1039)

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 Db 473 GACGGATTCAAGTGAAAGTAGCGGTCAAGAACGCCAAATCCACG 532

Qy 21 AsntrytlycSserserGluGlyCysSerVallysArgVallysGluGly 40
 Db 533 AACTACTACCCTGTCTGGGGCTGGGGCTGAAGAGCGGTGAGGGACCC 592

Qy 41 AspAspAlalaAlaTyrValleThrTyrGluGlyValHis 54
 Db 593 GACGACCCCCGTACGTATCACCACTAACGACGGCGTCAC 634

RESULT 6
 US-10-314-780A-1531
 ; Sequence 1531, Application US/10374780A
 ; Publication No. US2004019927A1

Page 4

GENERAL INFORMATION:

APPLICANT: Sherman, Bradley K
 APPLICANT: Riechmann, Jose Luis
 APPLICANT: Jiang, Cai-Zhong
 APPLICANT: Heard, Jacqueline E
 APPLICANT: Haake, Volker
 APPLICANT: Creelman, Robert A
 APPLICANT: Ratcliffe, Oliver
 APPLICANT: Adam, Luc J
 APPLICANT: Reuber, T. Lynne
 APPLICANT: Keddie, James
 APPLICANT: Brown, Pierre B
 APPLICANT: Pilgrim, Marsha L
 APPLICANT: Dubell III, Arnold T
 APPLICANT: Pineda, Omaira
 APPLICANT: Yu, Guo-Liang

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

FILE REFERENCE: MBI-0047 CIP

CURRENT APPLICATION NUMBER: US/10/374,780A

CURRENT FILING DATE: 2003-02-25

PRIOR APPLICATION NUMBER: 09/837,944

PRIOR FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: 60/310,847

PRIOR FILING DATE: 2001-08-09

PRIOR APPLICATION NUMBER: 09/934,455

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/336,049

PRIOR FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/338,692

PRIOR FILING DATE: 2001-12-11

PRIOR APPLICATION NUMBER: 10/171,468

PRIOR FILING DATE: 2002-06-14

PRIOR APPLICATION NUMBER: 10/225,066

PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: 10/225,067

PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: 10/225,068

PRIOR FILING DATE: 2002-08-09

NUMBER OF SEQ ID NOS: 2906

SOFTWARE: PatentIn version 3.2

SEQ ID NO: 1531

LENGTH: 1663

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Predicted polypeptide sequence is orthologous to S-10-374-780A-1531

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| best Local Similarity: | 81.48% | Mismatches: | 6 |
| query Match: | 83.56% | Indels: | 0 |
| B: | 17 | Gaps: | 0 |

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| red. | No.: | Length: | 1663 |
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| y | 1 AspGlyPheLysTrpArgLysTrpArgLysSerValLysAsnAsnIleA | 7.35e-27 | |
| b | 1078 GACGGATTCACTGGGAAGTACCGGAGAGGGTCAGAACGCCAA | 249.00 | |
| y | 21 AsnTyrTrpLysCysSerSerGluGlyCysSerValLysLysBArgValGluA | 88.89% | |
| b | 1138 AACTAACCCCTGCAGGGCTGCCTACCATCCACTCATCACGCCGTCCAC | 81.48% | |
| y | 41 AspAspAlaAlaTyrValIleThrTrpCysLysGluValWlkis | 83.56% | |
| b | 1198 GACGACCCCCCTACSTCATCACACCTACGCGGTCTGAGAGGGTGTGAA | 17 | |

Sequence 1621, Application US/10412699B

Sequence 1621-699B-1-621

RESULT 7

Db 1198 |||||||GACGACCCCCCTACTGCTATCACCCTAGCAGCGTCCAC 1239
RESULT 8
 Sequence 1613, Application US/10412699B
 Publication No. US20040045049A1
 GENERAL INFORMATION:
 APPLICANT: Mendel Biotechnology, Inc.
 APPLICANT: Zhang, James
 APPLICANT: Promm, Michael E.
 APPLICANT: Heard, Jacqueline B.
 APPLICANT: Riechmann, Jose Luis
 APPLICANT: Adam, Luc J.
 APPLICANT: Broun, Pierre E.
 APPLICANT: Pineda, Omaira
 APPLICANT: Reuber, T. Lynne
 APPLICANT: Keddie, James S.
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Jiang, Cai-Zhong
 APPLICANT: Samaha, Raymond R.
 APPLICANT: Pilgrim, Marsha L.
 APPLICANT: Creelman, Robert A.
 APPLICANT: DuBell, Arnold N.
 APPLICANT: Ratcliffe, Oliver
 APPLICANT: Kumimoto, Roderick
 APPLICANT: Sherman, Bradley K.
 TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
 FILE REFERENCE: MBI-0048CIP
 CURRENT APPLICATION NUMBER: US/10/412,699B
 CURRENT FILING DATE: 2003-04-10
 PRIOR APPLICATION NUMBER: 09/594,519
 PRIOR FILING DATE: 1999-09-13
 PRIOR APPLICATION NUMBER: 09/439,376
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: 09/506,720
 PRIOR APPLICATION NUMBER: 09/513,030
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/533,392
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/533,029
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/532,591
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/533,648
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: 09/713,994
 PRIOR FILING DATE: 2000-11-16
 PRIOR APPLICATION NUMBER: 09/819,142
 PRIOR FILING DATE: 2001-03-27
 REMAINING Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 2011
 SOFTWARE: PatentIn version 3.2
 LENGTH: 680
 TYPE: DNA
 ORGANISM: Zea mays
 US-10-412-699B-1613

Qy 21 AsnTyrrTyrLysCysSerSerGluGlyCysSerValLysBargValGluArgAspGly 40
 Db 117 AACTACTACGGGTCTAACGGAGGGTCAAGTGTGAGAGGGTGTGAGCTACGGATGCAC 176
RESULT 9
 US-10-412-699B-1612
 ; Sequence 1612, Application US/10412699B
 ; GENERAL INFORMATION:
 ; APPLICANT: Mendel Biotechnology, Inc.
 ; APPLICANT: Zhang, James
 ; APPLICANT: Fromm, Michael E.
 ; APPLICANT: Head, Jacqueline B.
 ; APPLICANT: Riechmann, Jose Luis
 ; APPLICANT: Adam, Luc J.
 ; APPLICANT: Broun, Pierre E.
 ; APPLICANT: Pineda, Omaira
 ; APPLICANT: Reuber, T. Lynne
 ; APPLICANT: Keddie, James S.
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Jiang, Cai-Zhong
 ; APPLICANT: Samaha, Raymond R.
 ; APPLICANT: Pilgrim, Marsha L.
 ; APPLICANT: Creelman, Robert A.
 ; APPLICANT: DuBell, Arnold N.
 ; APPLICANT: Ratcliffe, Oliver
 ; APPLICANT: Kumimoto, Roderick
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
 ; FILE REFERENCE: MBI-0048CIP
 ; CURRENT APPLICATION NUMBER: US/10/412,699B
 ; CURRENT FILING DATE: 2003-04-10
 ; PRIOR APPLICATION NUMBER: 09/394,519
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: 09/489,376
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: 09/506,720
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 09/533,030
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/533,392
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/533,029
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/532,591
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/533,648
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/713,994
 ; PRIOR FILING DATE: 2000-11-16
 ; PRIOR APPLICATION NUMBER: 09/819,142
 ; PRIOR FILING DATE: 2001-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 2011
 ; SOFTWARE: PatentIn version 3.2
 ; LENGTH: 743
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; US-10-412-699B-1612
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 Pred. No.: 3.1e-27 Length: 680
 Score: 248.00 Matches: 42
 Percent Similarity: 92.59% Conservative: 8
 Best Local Similarity: 77.78% Mismatches: 4
 Query Match: 83.22% Indels: 0
 DB: 18 Gaps: 0
 US-10-666-642-194_COPY_111_164 (1-54) x US-10-412-699B-1613 (1-680)
RESULT 10
 Qy 1 AspGlyPhenylsTrpArgLysTrpGlyLysSsSerValLysBargValGluArgAspGly 20
 Db 57 GACGGCTACAGTGAGGAAGTCCGTCAGAACGCCAACAAAG 116

US-10-666-642-194_COPY_111_164 (1-54) x US-10-412-699B-1612 (1-743)

Qy 1 AspGlyPhenylSerParglyStryGlyLysSlysSerVallysAsnAsnIleAsnLysArg 20
Db 18 GAGGCTTACAACTGGAGAATGACGGAAAGTCGGTCARGAACAGCCAAACCCAAAGG 77

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerVallysArgValGluArgAspGly 40
Db 78 AACTACTACCGTGCTGCAAGCGAAGCTGAACTGAAAGAGGGCTGGGGGAAACAG 137

Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
Db 138 GAGGACCCCAGTACGTGTTGACGACTACAGGGATGAC 179

RESULT 10
US-10-425-115-93169
; Sequence 93169, Application US/10425115
; Publication No. US2004021427A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO: 93169
; LENGTH: 902
; TYPE: DNA
; FEATURE:
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: MRT4577_184958C.1
US-10-425-115-93169

Alignment Scores:
Pred. No.: 3.88e-27 Length: 802
Score: 248.00 Matches: 42
Percent Similarity: 92.59% Conservative: 8
Best Local Similarity: 77.78% Mismatches: 4
Query Match: 83.22% Indels: 0
DB: 20 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-425-115-93169 (1-802)

Qy 1 AspGlyPhenylSerParglyStryGlyLysSlysSerVallysAsnAsnIleAsnLysArg 20
Db 57 GAGGCTTACAACTGGAGAATGACGGAAAGTCGGTCARGAACAGCCAAACCCAAAGG 116

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerVallysArgValGluArgAspGly 40
Db 117 AACTACTACCGTGCTGCAAGCGAAGCTGAAAGACGGGCTGGACGGGAAACAG 176

Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
Db 177 GAGGACCCCAGTACGTGTTGACGACTACAGGGATGAC 218

RESULT 11
US-10-437-963-63714
; Sequence 63714, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 63714
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_6492C.1
US-10-437-963-63714

Alignment Scores:
Pred. No.: 4.26e-27 Length: 666
Score: 247.00 Matches: 42
Percent Similarity: 90.74% Conservative: 7
Best Local Similarity: 77.78% Mismatches: 5
Query Match: 82.89% Indels: 0
DB: 19 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-437-963-63714 (1-666)

Qy 1 AspGlyPhenylSerParglyStryGlyLysSlysSerVallysAsnAsnIleAsnLysArg 20
Db 406 GAGGCTTACAGTGGCAAGTACGGTCAAGTCAGAACGCCAAACCCAAAGG 465

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerVallysArgValGluArgAspGly 40
Db 466 AACATCATACCGTGCTGACGGAACTGTCACCTGAAGAAGACGGTGGAGGGACAGG 525

Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
Db 526 GAGGACCCCAGTACGTGTTGACGACTACAGGGACGSCAC 567

RESULT 12
US-10-425-114-10354
; Sequence 10354, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; SEQ ID NO: 93128
; LENGTH: 952
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700905693_FLI
US-10-425-114-10354

Alignment Scores:
Pred. No.: 6.92e-27 Length: 952
Score: 247.00 Matches: 45
Percent Similarity: 90.74% Conservative: 4
Best Local Similarity: 83.33% Mismatches: 5
Query Match: 82.89% Indels: 0
DB: 18 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-425-114-10354 (1-952)

Qy 1 AspGlyPhenylSerParglyStryGlyLysSlysSerVallysAsnAsnIleAsnLysArg 20

Db 376 GATGGATACTAACAGTGGGAAAGTACGGCAACAGTCGTGAGGACAGTCGCCAATCTAAGG 435
 Qy 21 Asn^{Tyr} Tyr^{Ser} Ser^{Glu} Gly^{Ser} Val^{Lys} Arg^{Val} Glu^{Arg} Asp^{Gly} 40
 Db 436 AACACTAACATGTCAGTGGGATGCAAGTGGTGAAGAAAAGGTGAAAGGTAGATA 495

Qy 41 ASP^{Ala} Lys^{Val} Ile^{Thr} Thr^{Glu} Gly^{Ile} His 54
 Db 496 GATGACTACGCTACTGTGATAACACATATGAAGTGTGCAC 537

RESULT 13
 US-10-424-599-115917
 / Sequence 115917, Application US/10424599
 / Publication No. US20040031072A1
 / GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovacic David K
 ; APPLICANT: Zhou Yihua
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO: 115917
 ; LENGTH: 974
 ; TYPE: DNA
 ; FEATURE: ORGANISM: Glycine max
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_75684C.1
 ; US-10-424-599-115917

Alignment Scores:
 Pred. No.: 7.13e-27 Length: 974
 Score: 247.00 Matches: 45
 Percent Similarity: 90.74% Conservative: 4
 Best Local Similarity: 83.33% Mismatches: 5
 Query Match: 82.89% Indels: 0
 DB: 393 GATGGATACTAACAGTGGGAGTAGCGCAACAGTGGTGAAGAAAAGGTGAAAGGTAGATA 452

US-10-666-642-194_COPY_111_164 (1-54) x US-10-424-599-115917 (1-974)
 Qy 1 Asp^{Gly} Phe^{Lys} Trp^{Arg} Lys^{Tyr} Gly^{Ser} Val^{Lys} Arg^{Asn} Asn^{Leu} Asn^{Lys} Arg 20
 Db 393 GATGGATACTAACAGTGGGAGTAGCGCAACAGTGGTGAAGAAAAGGTGAAAGGTAGATA 512

Qy 21 Asn^{Tyr} Tyr^{Ser} Ser^{Glu} Gly^{Ser} Val^{Lys} Arg^{Val} Glu^{Arg} Asp^{Gly} 40
 Db 453 AACACTAACATGTCAGTGGGATGCAAGTGGTGAAGAAAAGGTGAAAGGTAGATA 554

RESULT 14
 US-10-412-699B-1609/c
 / Sequence 1609, Application US/10412699B
 / Publication No. US20040045049A1
 / GENERAL INFORMATION:
 ; APPLICANT: Mendel Biotechnology, Inc.
 ; APPLICANT: Zhang, James
 ; APPLICANT: Fromm, Michael E.
 ; APPLICANT: Heard, Jacqueline E.
 ; APPLICANT: Riechmann, Jose Luis
 ; APPLICANT: Adam, Luc J.
 ; APPLICANT: Broun, Pierre E.
 ; APPLICANT: Pineda, Omaira
 ; APPLICANT: Reuber, T. Lynne
 ; APPLICANT: Keddie, James S.
 ; APPLICANT: Yu, Guo-Jiang
 ; APPLICANT: Jiang, Cai-Zhong
 ; APPLICANT: Samaha, Raymond R.

; APPLICANT: Pilgrim, Marsha L.
 ; APPLICANT: Creelman, Robert A.
 ; APPLICANT: Dubell, Arnold N.
 ; APPLICANT: Ratcliffe, Oliver
 ; APPLICANT: Kumimoto, Roderick K.
 ; APPLICANT: Sherman, Bradley K.
 ; FILE REFERENCE: MBI-0048CIP
 ; CURRENT APPLICATION NUMBER: US/10/412-699B
 ; CURRENT FILING DATE: 2003-04-10
 ; PRIOR APPLICATION NUMBER: 09/394,519
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: 09/489,376
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: 09/506,720
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 09/533,030
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/533,392
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/533,029
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/532,591
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/533,648
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/533,029
 ; PRIOR FILING DATE: 2000-11-16
 ; PRIOR APPLICATION NUMBER: 09/819,142
 ; PRIOR FILING DATE: 2001-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 2011
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 1609
 ; LENGTH: 974
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; US-10-412-699B-1609

Alignment Scores:
 Pred. No.: 7.13e-27 Length: 974
 Score: 247.00 Matches: 45
 Percent Similarity: 90.74% Conservative: 4
 Best Local Similarity: 83.33% Mismatches: 5
 Query Match: 82.89% Indels: 0
 DB: 18 GDB: 0
 ; GDB8:

US-10-666-642-194_COPY_111_164 (1-54) x US-10-412-699B-1609 (1-974)
 Qy 1 Asp^{Gly} Phe^{Lys} Trp^{Arg} Lys^{Tyr} Gly^{Ser} Val^{Lys} Arg^{Asn} Asn^{Leu} Asn^{Lys} Arg 20
 Db 582 GATGGATACTGGGAGTAGCGCAACAGTGGTGAAGAAAAGGTGAAAGGTAGATA 523

Qy 21 Asn^{Tyr} Tyr^{Ser} Ser^{Glu} Gly^{Ser} Val^{Lys} Lys^{Ser} Arg^{Val} Glu^{Arg} Asp^{Gly} 40
 Db 522 AACCTACTAACAGCTACTGTGATAACACATATGAAGTGTGCAC 554

RESULT 15
 US-10-425-115-74300
 / Sequence 74300, Application US/10425115
 ; Publication No. US20040214272A1
 / GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 363326
SEQ ID NO 74300
LENGTH: 580
TYPE: DNA.
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_167760C.1
S-10-425-115-74300

| Alignment Scores: | | JS-10-666-642-194_COPY_111_164 (1-54) x US-10-425-115-74300 (1-580) | | | | | |
|---------------------------|--------|---|-----|--|--|--|--|
| Score: | 1e-26 | Length: | 580 | | | | |
| Score: | 244.00 | Matches: | 43 | | | | |
| Percent Similarity: | 88.89% | Conservative: | 5 | | | | |
| Percent Local Similarity: | 79.63% | Mismatches: | 6 | | | | |
| Query Match: | 81.88% | Indels: | 0 | | | | |
| BB: | 20 | Gaps: | 0 | | | | |
| | | 1 AspGlyPhelystStrpargLysTyrGlyLysBsrSerrvallysAsnIleasnLysArg | 20 | | | | |
| YY | | 389 GATGGATTCATAGTGGAAAGTATGCCAAGGGCTGTCAGAGTGCCCAAATCAGG | 448 | | | | |
| bb | | 21 AsnTyrTyrLysCysSerSerLysGluGlyCysserVallysArgValGluArgAspGly | 40 | | | | |
| YY | | 449 AACTACTACCGTGCTGTGCGAGGCTGCGCGTGAAGAGCGCTGGAGGGACCGC | 508 | | | | |
| bb | | 41 AspAspAlaAlaTyrValleThrThrTyrGluGlyValHis | 54 | | | | |
| YY | | 509 GACGACCCCCGGTAACTCTCATACCCACCTAACAGGCGTCCAC | 550 | | | | |
| bb | | | | | | | |

Search completed: August 26, 2005, 05:03:58
Job time: 527 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 25, 2005, 23:29:33 ; Search time 140 Seconds
(without alignments)

631.135 Million cell updates/sec

Title: US-10-666-642-194_COPY_111_164

Perfect score: 298

Sequence: 1 DGFKWKYGKSVKNNIKR.....RVERDDAAVVITYEGVH 54

Scoring table: BLOSUM62

Xgapop 10.0 ; Xgapext 0.5

Ygapop 10.0 ; Ygapext 0.5

Fgapop 6.0 ; Fgapext 7.0

Delp 6.0 ; Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0⁺

Maximum Match 10⁺

Listing first 45 summaries

Command line parameters:

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-Q=cgn2_1/USPFTO_spool/US1666642/rutat_25082005_130054_24882/app_query.fasta_1.199
-DB=issued_Patent_NA -QMT=fastap -SUFFIX=rna -MINMATCH=0.1 -LOCFCII=0
-LOCPEXT=0 -UNITS=Dists -START=1 -END=-1 -MATRIX=1blosum62 -TRANS=human40.cdi
-LIST=45 -DOCOLIGN=200 -THR SCORE=DCP -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORH=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=USR-US1666642 @CCN:pt0 -WARN=0 -LONGLOG
-NO MMAP -LARGESEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -TIMEOUT=30 -THREADS=1 -XGAPOP=1.0 -KGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Issued_Patent_NA:*

- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq/*
- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq/*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq/*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq/*
- 5: /cgn2_6/prodata/1/ina/PCUTUS_COMB.seq/*
- 6: /cgn2_6/prodata/1/ina/backfile1.seq/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | Match | Length | DB ID | Description |
|------------|-------|-------|--------|-----------------------|--------------------|
| 1 | 242 | 81.2 | 352 | 4 US-09-640-211A-1204 | Sequence 1204, Ap |
| 2 | 230 | 77.2 | 748 | 4 US-09-533-029-29 | Sequence 29, App1 |
| 3 | 197 | 66.1 | 724 | 4 US-09-533-029-15 | Sequence 15, App1 |
| 4 | 191 | 64.1 | 471 | 4 US-09-640-211A-1406 | Sequence 1406, Ap |
| 5 | 190 | 63.8 | 878 | 4 US-09-533-029-116 | Sequence 116, App1 |
| 6 | 187 | 62.8 | 527 | 4 US-09-640-211A-1849 | Sequence 1849, Ap |
| 7 | 165 | 55.4 | 378 | 4 US-09-640-211A-1841 | Sequence 1841, Ap |
| 8 | 158 | 52.9 | 306 | 4 US-09-313-294A-059 | Sequence 4059, Ap |
| 9 | 157.5 | 52.9 | 162 | 4 US-09-640-211A-1219 | Sequence 2119, Ap |
| 10 | 154.5 | 51.3 | 296 | 4 US-09-640-211A-1509 | Sequence 1509, Ap |
| 11 | 153.5 | 51.5 | 1130 | 4 US-09-533-029-27 | Sequence 27, App1 |
| 12 | 153.5 | 51.5 | 561 | 4 US-09-640-211A-1580 | Sequence 1580, Ap |

ALIGMENTS

| RESULT 1 | Score: 1204 | Length: 352 |
|--------------------------------|---|-----------------|
| US-09-640-211A-1204 | Score: 1204, Application US/09640211A | Matches: 43 |
| | Percent Similarity: 85.19% | Conservative: 3 |
| | Best Local Similarity: 79.33% | Mismatches: 8 |
| | Query Match: 81.21% | Indels: 0 |
| | DB: 4 | Gaps: 0 |
| US-10-666-642-194_COPY_111_164 | Score: 10-666-642-194_COPY_111_164 (1-54) × US-09-640-211A-1204 (1-352) | |
| Qy | 1 AspGlyPhenylalanylarginylglycyllysylservalylasparagine | |
| Db | 184 GACGGATTCAAGTSGAGGATACCGGAGAACGTTGAGAACGTCGAXTCGAGG | 243 |

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysSArgValGluArgAspGly 40
 Db 244 Aspartic Acid Tryptophan Threonine Alanine Glutamic Acid Cysteine Asparagine 303

Qy 41 AspAspAlaAlaTyrValIleThrThrThrGluGlyValHis 54
 Db 304 GAGGCCAAAGGTATGATAACATACGAGCTCAT 345

RESULT 2
 US-09-533-029-29
 / Sequence 29, Application US/09533029
 / Patent No. 6664446
 / GENERAL INFORMATION:
 / APPLICANT: Heard, Jacqueline
 / APPLICANT: Broun, Pierre
 / APPLICANT: Keddie, Jose-Luis
 / APPLICANT: Riechmann, Oliver
 / APPLICANT: Pineda, Omaira
 / APPLICANT: Adam, Luc Raymond
 / APPLICANT: Samaha, Raymond
 / APPLICANT: Jiang, Cai-Zhong
 / APPLICANT: Reuber, Lynne
 / TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
 / FILE REFERENCE: MBI-010
 / CURRENT APPLICATION NUMBER: US/09/533, 029
 / CURRENT FILING DATE: 2000-03-22
 / EARLIER APPLICATION NUMBER: 60/125, 814
 / EARLIER FILING DATE: 1999-03-23
 / NUMBER OF SEQ ID NOS: 121
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 15
 / LENGTH: 724
 / TYPE: DNA
 / ORGANISM: Arabidopsis thaliana
 / FEATURE:
 / OTHER INFORMATION: G179
 / US-09-533-029-15

Alignment Scores:
 Pred. No.: 1.34e-20
 Score: 197.00
 Percent Similarity: 79.3%
 Best Local Similarity: 61.11%
 Query Match: 66.11%
 DB: 4
 Length: 724
 Matches: 33
 Conservatve: 10
 Mismatches: 11
 Indels: 0
 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-15 (1-724)

Qy 1 AspGlyPheLysTrpArgLysTrpGlyLysSerValLysAsnAsnLeasnLysArg 20
 Db 263 GATGGATACAGTTGGAGGAGTACGCCAAAGCAGTCAGAACATCCATTCAGGG 322

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysSArgValGluArgAspGly 40
 Db 323 AGCTATTATAAGTGCAGAGAGAGTCAGACTGAGAGCGAGCAATGAGGCAATGG 382

Qy 41 AspAspAlaAlaTyrValIleThrThrGluGlyValHis 54
 Db 383 GGAGGCGANGGAGTGTCGACCACATACCAAGCTTGTCTCAT 424

RESULT 4
 US-09-640-211A-1406
 / Sequence 1406, Application US/09640211A
 / Patent No. 6833446
 / GENERAL INFORMATION:
 / APPLICANT: Wood, Marion A.
 / APPLICANT: Shenk, Michael A.
 / APPLICANT: McGrath, Annette E.
 / APPLICANT: Gleim, Matthew
 / TITLE OF INVENTION: Modification of Gene Transcription
 / FILE REFERENCE: 11000-1021C1U
 / CURRENT APPLICATION NUMBER: US/09/640,211A
 / CURRENT FILING DATE: 2000-08-16
 / NUMBER OF SEQ ID NOS: 2368
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 1406
 / LENGTH: 471
 / TYPE: DNA
 / ORGANISM: Eucalyptus grandis

Alignment Scores:
 Pred. No.: 6.05e-20
 Score: 191.00
 Percent Similarity: 77.78%
 DB-09-640-211A-1406

RESULT 3
 US-09-533-029-15
 / Sequence 15, Application US/09533029
 / GENERAL INFORMATION:
 / APPLICANT: Heard, Jacqueline
 / APPLICANT: Broun, Pierre
 / APPLICANT: Riechmann, Oliver
 / APPLICANT: Keddie, Jose-Luis
 / APPLICANT: James

```

Best Local Similarity: 61.11% Mismatches: 12
Query Match: 64.09% Indels: 0
DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1406 (1-471)

Qy 1 AspGlyPhelbySrpArgLysTerGlyLysbServallySasnDnlleasnLyBarg 20
Db 233 GATGGTACAATGGGACTACGCCAGAACGTCCTGAAACGCCCTCACCCAGA 292

Qy 21 AsnTyTyrlsCysSerSerGluGlyCysServallySlysArgValGluArgPgly 40
Db 293 AGTTAACCTGCATCAGTAATTGCGAGTAGGTAGAGGAGGGTCAGCGGTTGCG 352

Qy 41 ASPASpalaatTyVallethrThrtyrGluGlyValHis 54
Db 353 GAAGATGTCGATGCTGATAACGACTACAGGGCAGCAT 394

RESULT 5
US-09-533-029-116
; Sequence 116, Application US/09533029
; Patent No. 664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 116
; LENGTH: 878
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1274
US-09-533-029-116

Alignment Scores:
Pred. No.: 1.45e-19 Length: 878
Score: 191.00 Matches: 35
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.09% Indels: 0
DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-116 (1-878)

Qy 20 ArgAspAspAlaAlaTyvallethrThrGluGlyCysServallySlysArgValGluArgAsp 39
Db 687 AGGAATTACATCAACGCTCAAGTGAAGGTTGCTCGTGAGAAGGGTGTCCAT 746

Qy 40 GlyAspAspAlaAlaTyvallethrThrGluGlyValHis 54
Db 747 GGTGAGATGGAGCTTATGTAATTACACATGAGGAATGTCAT 791

RESULT 6
US-09-640-211A-1849
; Sequence 1849, Application US/09640211A

```

```

; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09-640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 1849
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-1849

Alignment Scores:
Pred. No.: 1.01e-19 Length: 527
Score: 190.00 Matches: 33
Percent Similarity: 79.63% Conservative: 10
Best Local Similarity: 61.11% Mismatches: 11
Query Match: 63.76% Indels: 0
DB: 4 Gaps: 0

US-09-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1849

Qy 1 ArgGlyPhenylalanylSerGlyStryGlyLysSerValLysAla
Db 214 GATGGCTPATAGTGGCAAATATGGCCAAAGCTGTCAAAAC

Qy 21 AsnTyrItyLyscysSerSerGluGlycysSerValLysBarg
Db 274 AGTTACTATCGTGTGACAATGAAAATGCTCATGGRAGAGA

Qy 41 AspAspAlaAlaTyrValileThrItyArgLysGlyValHis 54
Db 334 GAGATCCAGGAATTGTCATTAGCACATATGAGGACGCT 37

RESULT 7
US-09-640-211A-1841
; Sequence 1841, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09-640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 1841
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-1841

Alignment Scores:
Pred. No.: 1.81e-19 Length: 378
Score: 187.00 Matches: 33
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 61.11% Mismatches: 14
Query Match: 62.75% Indels: 0
DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1841

```

Qy 1 AspGlyPhelYstPArgLysTyrGlyLysSrvValLysAsnAlleAsnLysArg 20
 Db 92 GATGGPATATGGTCCAGATGGCAGATGGCATGAACTGAACTGAACTCAAGG 151
 ; SEQ ID NO: 1219
 ; LENGTH: 162
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 US-09-640-211A-1219

Alignment Scores:
 Pred. No.: 1.49e-15 Length: 162
 Score: 158.00 Matches: 28
 Percent Similarity: 74.47% Conservative: 7
 Best Local Similarity: 59.57% Mismatches: 12
 Query Match: 53.02% Indels: 0
 DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1219 (1-162)

Qy 1 AspGlyPhelYstPArgLysTyrGlyLysSrvValLysAsnAlleAsnLysArg 20
 Db 20 GATGGTATGGCTGCAGATGGCAGATGGCATGAACTGAACTCAAGG 79
 ; SEQ ID NO: 1219
 ; LENGTH: 162
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 US-09-640-211A-1219

Alignment Scores:
 Pred. No.: 1.49e-15 Length: 162
 Score: 158.00 Matches: 28
 Percent Similarity: 74.47% Conservative: 7
 Best Local Similarity: 59.57% Mismatches: 12
 Query Match: 53.02% Indels: 0
 DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1219 (1-162)

Qy 21 AsnTYrrTyrrLysCysSerGluGlyCysSrvValLysAsnAlleAsnLysArg 20
 Db 152 AGTACTATAATGCAAAATGTGGATTCAGATGGAAACATGGAAAGGATCA 211
 ; SEQ ID NO: 1219
 ; LENGTH: 162
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 US-09-640-211A-1219

Alignment Scores:
 Pred. No.: 1.49e-15 Length: 162
 Score: 158.00 Matches: 28
 Percent Similarity: 74.47% Conservative: 7
 Best Local Similarity: 59.57% Mismatches: 12
 Query Match: 53.02% Indels: 0
 DB: 4 Gaps: 0

RESULT 8

US-09-313-294A-4059

Sequence 4059, Application US/09313294A
 Patent No. 6476212
 GENERAL INFORMATION:
 APPLICANT: Lalngudi, Raghunath V.
 APPLICANT: Ito, Laura Y.
 APPLICANT: Sherman, Bradley K.
 APPLICANT: Sherman, Michael A.
 TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 FILE REFERENCE: PL-0017 US
 CURRENT APPLICATION NUMBER: US/09/313,294A
 CURRENT FILING DATE: 1999-05-14
 NUMBER OF SEQ ID NOS: 7600
 SOFTWARE: PERL Program
 SEQ ID NO: 4059
 LENGTH: 306
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE: misc feature
 NAME/KEY: misc feature
 OTHER INFORMATION: Insayte ID NO. 6476212 7003477613H1
 US-09-313-294A-4059

Alignment Scores:
 Pred. No.: 3.1e-16 Length: 306
 Score: 165.00 Matches: 33
 Percent Similarity: 74.07% Conservative: 7
 Best Local Similarity: 61.11% Mismatches: 14
 Query Match: 55.37% Indels: 1
 DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-313-294A-4059 (1-306)

Qy 1 AspGlyPhelYstPArgLysTyrGlyLysSrvValLysAsnAlleAsnLysArg 20
 Db 97 GATGGPATATGGTGGCCAAATAATGCCAGAAAGTACTGAAGAAACCGG 156
 ; SEQ ID NO: 1219
 ; LENGTH: 162
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 US-09-640-211A-1219

Alignment Scores:
 Pred. No.: 4.13e-15 Length: 296
 Score: 157.50 Matches: 30
 Percent Similarity: 70.31% Conservative: 8
 Best Local Similarity: 55.56% Mismatches: 15
 Query Match: 52.85% Indels: 1
 DB: 4 Gaps: 1

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1509 (1-296)

Qy 1 AspGlyPhelYstPArgLysTyrGlyLysSrvValLysAsnAlleAsnLysArg 20
 Db 83 GATGGTATGGCTGGAGGATGGTGGAAATGTGCAATGTGCAATGTGCA 139
 ; SEQ ID NO: 1219
 ; LENGTH: 139
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 US-09-640-211A-1509

Alignment Scores:
 Pred. No.: 4.13e-15 Length: 296
 Score: 157.50 Matches: 30
 Percent Similarity: 70.31% Conservative: 8
 Best Local Similarity: 55.56% Mismatches: 15
 Query Match: 52.85% Indels: 1
 DB: 4 Gaps: 1

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1509 (1-296)

Qy 21 AsnTYrrTyrrLysCysSerGluGlyCysSrvValLysAsnAlleAsnLysArg 20
 Db 140 AGCTACTATAGATGCAACCTGCTGCAATGTGCAATGTGCAATGTGCA 199
 ; SEQ ID NO: 1219
 ; LENGTH: 199
 ; TYPE: DNA
 ; ORGANISM: Eucalyptus grandis
 US-09-640-211A-199

Alignment Scores:
 Pred. No.: 4.13e-15 Length: 296
 Score: 157.50 Matches: 30
 Percent Similarity: 70.31% Conservative: 8
 Best Local Similarity: 55.56% Mismatches: 15
 Query Match: 52.85% Indels: 1
 DB: 4 Gaps: 1

RESULT 9

US-09-640-211A-1219

Sequence 1219, Application US/09640211A
 Patent No. 6833446
 GENERAL INFORMATION:
 APPLICANT: Wood, Marion
 APPLICANT: McGrath, Annette
 APPLICANT: Glenn, Matthew
 TITLE OF INVENTION: Compositions and Methods for the
 Modification of Gene Transcription
 FILE REFERENCE: 1100.1021CU
 CURRENT APPLICATION NUMBER: US/09/640,211A
 CURRENT FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 2368
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1219

RESULT 11

US-09-640-211A-1219

Sequence 1219, Application US/09640211A
 Patent No. 6833446
 GENERAL INFORMATION:
 APPLICANT: Wood, Marion
 APPLICANT: McGrath, Annette
 APPLICANT: Glenn, Matthew
 TITLE OF INVENTION: Compositions and Methods for the
 Modification of Gene Transcription
 FILE REFERENCE: 1100.1021CU
 CURRENT APPLICATION NUMBER: US/09/640,211A
 CURRENT FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 2368
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1219

US-09-533-029-27
 Sequence 27, Application US/09533029
 Patent No. 6664446
 GENERAL INFORMATION:
 APPLICANT: Heard, Jacqueline
 APPLICANT: Broun, Pierre
 APPLICANT: Riechmann, Jose-Luis
 APPLICANT: Keddie, James
 APPLICANT: Pineda, Omaira
 APPLICANT: Adam, Luc
 APPLICANT: Samaha, Raymond
 APPLICANT: Zhang, James
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Ratcliffe, Oliver
 APPLICANT: Pilgrim, Marsha
 APPLICANT: Jiang, Cai-Zhong
 APPLICANT: Reuber, Lynne
 TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
 FILE REFERENCE: MBI-010
 CURRENT APPLICATION NUMBER: US/09/533,029
 CURRENT FILING DATE: 2000-03-22
 EARLIER APPLICATION NUMBER: 60/125,814
 EARLIER FILING DATE: 1999-03-23
 NUMBER OF SEQ ID NOS: 121
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 27
 LENGTH: 1130.
 TYPE: DNA
 ORGANISM: *Arabidopsis thaliana*

FEATURE:
 OTHER INFORMATION: G291

FEATURE:
 OTHER INFORMATION: "n" bases at various positions throughout the
 US-09-533-029-27

Alignment Scores:
 Pred. No.: 7.77e-14 Length: 1130
 Score: 154.50 Matches: 26
 Percent Similarity: 74.55% Conservative: 15
 Best Local Similarity: 47.27% Mismatches: 13
 Query Match: 51.85% Indels: 1
 DB: 4 Gaps: 1

US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-27 (1-1130)
 Qy 1 AspGlyPhenylsTrArglyStryGlyLyStrySvalValAsnAsnLeAsnLysArg 20
 Db 554 GATGGCTATCATGGAAATAATGACAGAAAGTGACTAGAGACATCCACAGA 613
 Qy 21 AsnTyTyrylStryCYSer--SerGluGlyCYSvalValValGluGargAsp 39
 Db 614 GCTTACTTCAAATGCTGCTCAAGGTGTTCTGTCAAAGAAGTTCAGAGAAGT 673
 Qy 40 GlyAspAspAlaAlaTyrValleThrThrTyrGluGlyValHis 54
 Db 674 GTGGGAGTAGTCGTTAGTGCAACTATGGGAAACAC 718

RESULT 12
 US-09-640-211A-1580
 Sequence 1580, Application US/09640211A
 Patent No. 6833446
 GENERAL INFORMATION:
 APPLICANT: Wood, Marion
 APPLICANT: McGrath, Annette
 APPLICANT: Glenn, Matthew
 APPLICANT: Shenk, Michael A.
 APPLICANT: McGrath, Annette
 APPLICANT: Glenn, Matthew
 TITLE OF INVENTION: Compositions and Methods for the
 Modification of Gene Transcription
 FILE REFERENCE: 11000.1021CU
 CURRENT APPLICATION NUMBER: US/09/640,211A
 CURRENT FILING DATE: 2000-08-16
 NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1580
 ; LENGTH: 561
 ; TYPE: DNA
 ; ORGANISM: *Pinus radiata*
 ; US-09-640-211A-1580
 Alignment Scores:
 Pred. No.: 4.14e-14 Length: 561
 Score: 153.50 Matches: 29
 Percent Similarity: 65.45% Conservative: 7
 Best Local Similarity: 52.73% Mismatches: 18
 Query Match: 51.51% Indels: 1
 DB: 4 Gaps: 1

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1580 (1-561)
 Qy 1 AspGlyPhenylsTrArglyStryGlyLyStrySvalValAsnAsnLeAsnLysArg 20
 Db 272 GATGAATTCCTATGGGAAATAATGGACAGAGGCCATTAAAGGCCTCTCCACATCCAGA 331
 Qy 21 AsnTyTyrylStryCYSer--SerGluGlyCYSvalValValGluGargAsp 39
 Db 332 GGTTATGAAATGCGACAGTGAGGTTGCCTGAGAAGGACAGTGAACGCGCC 391
 Qy 40 GlyAspAspAlaAlaTyrValleThrThrTyrGluGlyValHis 54
 Db 392 CTGGACGATGCCAACGATTGATTGATTGAAATGAGGGCAACAC 435

RESULT 13
 US-09-533-029-89
 Sequence 89, Application US/09533029
 ; Patent No. 666446
 ; GENERAL INFORMATION:
 ; APPLICANT: Heard, Jacqueline
 ; APPLICANT: Broun, Pierre
 ; APPLICANT: Riechmann, Jose-Luis
 ; APPLICANT: Keddie, James
 ; APPLICANT: Pineda, Omaira
 ; APPLICANT: Adam, Luc
 ; APPLICANT: Samaha, Raymond
 ; APPLICANT: Zhang, James
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Ratcliffe, Oliver
 ; APPLICANT: Pilgrim, Marsha
 ; APPLICANT: Jiang, Cai-Zhong
 ; APPLICANT: Reuber, Lynne
 ; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
 ; FILE REFERENCE: MBI-010
 ; CURRENT APPLICATION NUMBER: US/09/533, 029
 ; CURRENT FILING DATE: 2000-03-22
 ; EARLIER FILING DATE: 1999-03-23
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 89
 ; LENGTH: 1952
 ; TYPE: DNA
 ; ORGANISM: *Arabidopsis thaliana*
 ; FEATURE:
 ; OTHER INFORMATION: G186
 ; FEATURE:
 ; OTHER INFORMATION: "n" bases at various positions throughout the
 ; US-09-533-029-89
 Alignment Scores:
 Pred. No.: 4.8e-13 Length: 1952
 Score: 151.50 Matches: 28
 Percent Similarity: 70.31% Conservative: 11
 Best Local Similarity: 50.91% Mismatches: 15
 Query Match: 50.84% Indels: 1
 DB: 4 Gaps: 1

RESULT 14

US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-89 (1-1952)

Qy 1 AspGlyPhelystPargLysTyrGlyLysSerVallysAsnAsnIleAsnLysArg 20
 Db 1036 GATGGATGTCAATTGGAGAAATAATGCCAGAAGATGCCAAAGGGRATCCTTGTCCGGCG 1095

Qy 21 AsnTyrTyrLysCysSer--SerGluGlyCysserVallysLysArgValGluArgAsp 39
 Db 1096 GCATATACCGTCAGATGGCCAGGGTGTCCGGTTGCCAACAGTCAACGTTGC 1155

Qy 40 GlyAspAspAlaAlaTyrValleThrThrTyrGluGlyValHis 54
 Db 1156 GCGGAAGACAGATCAATTCTGATTACACCTACGAGGAACCAT 1200

RESULT 15

US-09-640-211A-1487

; Sequence 1487, Application US/09640211A

; Patent No. 6333446

; GENERAL INFORMATION:

; APPLICANT: Wood, Marion

; APPLICANT: Shenk, Michael A.

; APPLICANT: McGrath, Annette

; APPLICANT: Glenn, Matthew

; TITLE OF INVENTION: Compositions and Methods for the
Modification of Gene Transcription

; TITLE OF INVENTION: Modification of Gene Transcription

; FILE REFERENCE: 11000.1021CU

; CURRENT APPLICATION NUMBER: US/09/640,211A

; CURRENT FILING DATE: 2000-08-16

; NUMBER OF SEQ ID NOS: 2368

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1487

; LENGTH: 319

; TYPE: DNA

; ORGANISM: Eucalyptus grandis

US-09-640-211A-1487

Alignment Scores:
 Pred. No.: 3.12e-13 Length: 319
 Score: 145.50 Matches: 25
 Percent Similarity: 69.09% Conservative: 13
 Best Local Similarity: 45.45% Mismatches: 16
 Query Match: 48.83% Indels: 1
 DB: 4 Gaps: 1

US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-59 (1-1651)

Qy 1 AspGlyPhelystPargLysTyrGlyLysSerVallysAsnAsnIleAsnLysArg 20
 Db 749 GACGCGATGTCATGGAAATAATGGCAAAGGGAATCCATGTCTCGC 808

Qy 21 AsnTyrTyrLysCysSer--SerGluGlyCysserVallysLysArgValGluArgAsp 39
 Db 809 GCTTTATATCGTTGCACCATGGCCCTTGATGTCCTGAAACAGTCCACAGTGC 868

Qy 40 GlyAspAspAlaAlaTyrValleThrThrTyrGluGlyValHis 54
 Db 869 GCGGAAGGATACAATCTTGACAAACGTAAGGAACCAT 913

Search completed: August 26, 2005, 01:48:30
 Job time : 149 secs

RESULT 15

US-09-533-029-59

; Sequence 59, Application US/09533029

; Patent No. 664446

; GENERAL INFORMATION:

; APPLICANT: Heard, Jacqueline

; APPLICANT: Broun, Pierre

; APPLICANT: Riechmann, James

; APPLICANT: Keddie, James

; APPLICANT: Pineda, Omaira

; APPLICANT: Adam, Luc

; APPLICANT: Samaha, Raymond

; APPLICANT: Zhang, James

; APPLICANT: Yu, Guo-Liang

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 25, 2005, 19:45:28 ; Search time 2856 Seconds (without alignments)

916.170 Million cell updates/sec

Title: US-10-666-642-194_COPY_111_164

Pefect score: 98

Sequence: 1 DGFKWKRKYGKKSVKNNINKR.....RVERDGDDAAYVITYEGVH 54

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 10% Listing first 45 summaries

Command line parameters:

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-Q = Cgn 1 / USP0 spool / US 066642 / runat 25082005_130053_24856 / app query.fasta_1.199
-DB=GenEmb1 -QMT=fastap -SUFFIX=9e -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=-1 -END=-1 -MATRIXX=biosunm2 -TRANS=human40 .cdi -LIST=45
-DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US-10-666-642 @CCN 1.1 4200 @runat 25082005_130053_24856 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEQ SCORES=100 -DEPBLOCK=100 -LONGLOG
-DBT TIMEOUT=120 -WARN -NEQ -DELEXT=30 -THREADS=1 -XGAPOP=1.0 -XGAPEXT=0.5 -FGAPOP=6
-FGPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : GenEmb1;*

1: gb_ha:*

2: gb_ntg:*

3: gb_nin:*

4: gb_on:*

5: gb_ov:*

6: gb_dat:*

7: gb_db:*

8: gb_dl:*

9: gb_dp:*

10: gb_ro:*

11: gb_sts:*

12: gb_by:*

13: gb_un:*

14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB ID | Description |
|------------|-------|-------|--------------|-------|-------------|
| 1 | 298 | 100.0 | 585 | 8 | AF426252 |
| 2 | 242 | 81.2 | 707 | 8 | AK109578 |
| 3 | 242 | 81.2 | 792 | 8 | AK066252 |
| 4 | 242 | 81.2 | 839 | 8 | AY341854 |

FEATURES

| source | Location/Qualifiers |
|---------|--|
| 1. .585 | /organism="Arabidopsis thaliana" /mol type="mRNA" /db_xref="taxon:3702" /chromosome="V" /clone="BAC MXK3" /tissue_type="inflorescence" /ecotype="Columbia" |

ALIGNMENTS

| source | Location/Qualifiers |
|----------|--|
| 1. .585 | /organism="Arabidopsis thaliana" /mol type="mRNA" /db_xref="taxon:3702" /chromosome="V" /clone="BAC MXK3" /tissue_type="inflorescence" /ecotype="Columbia" |
| BT008482 | Arabidopsis sat |
| AY01224 | Arabidopsis Sequence |
| AY063870 | Arabidopsis |
| AC097112 | Oryza sat |
| AK06986 | Arabidopsis Sequence |
| AK52016 | Arabidopsis Sequence |
| BT008482 | Arabidopsis |
| AY01224 | Arabidopsis |
| BT002338 | Arabidopsis |
| AY114650 | Arabidopsis |
| AY062720 | Arabidopsis |
| AY136318 | Arabidopsis |
| LA113 | Cucumis sat |
| AP003341 | Oryza sat |
| AP003492 | Oryza sat |
| AY071849 | Arabidopsis |
| AK069091 | Oryza sat |
| AY241858 | Oryza sat |
| AY241859 | Oryza sat |
| AK53470 | Sequence |
| AF559793 | Oryza sat |
| D3038 | Ipomoea batatas |
| AK103745 | Oryza sat |
| AK065078 | Oryza sat |
| AK062027 | Oryza sat |
| AK054708 | Sequence |
| AK065518 | Oryza sat |
| AB026890 | Nicotiana |
| AB063576 | Nicotiana |
| AF404857 | Arabidopsis |

RESULT 1

| source | Location/Qualifiers |
|------------|---|
| AF426252 | 585 bp mRNA linear PLN 08-NOV-2001 |
| DEFINITION | Arabidopsis thaliana WRKY transcription factor 51 (WRKY51) mRNA, complete cds. |
| ACCESSION | AF426252 |
| VERSION | AF426252.1 GI:16798361 |
| KEYWORDS | Arabidopsis thaliana (thale cress) |
| SOURCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; euroids 1; Brassicales; Brassicaceae; Arabidopsis. |
| REFERENCE | 1 (bases 1 to 585) |
| AUTHORS | Kushnir, S., Ulker, B. and Somssich, I. B. |
| TITLE | Submitted (02-OCT-2001) Biochemistry, Max-Planck-Institut fur Zuchungsforschung, Carl-von-Linne-Weg 10, Koeln, NRW D-50829, Germany |

| | | | |
|--------------------------------|---|------------|---|
| gene | 1..585 /gene="WRKY51" 1..585 /genes="WRKY51" | AUTHORS | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanaogi,A., Hayashizaki,Y., Hara,I., Hara,T., Hayashida,K., Hayashiaki,Y., Hata,T., Hiraoka,T., Horii,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Hiramoto,K., Itoh,M., Kawamata,M., Kawamura,N., Kawai,J., Kogawa,I., Kanagawa,S., Katoh,H., Kawashima,N., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kikuchi,S., Kishikawa,T., Kishimoto,N., Kondo,S., Konno,H., Koudai,M., Kojima,K., Kurihara,C., Kurokawa,T., Kusumegi,T., Li,C., Lu,M., Kodama,T., Kojima,Y., Kondo,S., Konno,H., Koudai,M., Koya,S., Kurihara,C., Kurokawa,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,T., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narita,T., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohnsuki,K., Oka,M., Oota,H., Osato,N., Ota,Y., Otemo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakanoue,N., Sano,H., Sasaki,D., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sugabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Tomaru,A., Toyoda,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yamagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshihara,A. |
| | | TITLE | Submitted (27-AUG-2002) shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki, Japan (E-mail: skikuchi@niais.agric.go.jp) |
| | | JOURNAL | Tel: 81-29-838-7007; Fax: 81-29-838-7007 |
| | | COMMENT | This clone is one of the 28K full-length cDNA clones from rice. URL : http://cdna01.dna.agric.go.jp/cDNA/ |
| | | | NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yanada,H., Ooka,H., Hotta,I., Kohima,K., Namiiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Yamamoto,M. |
| | | | PAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurokawa,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Toshimura,A., Matsubara,K. and Murakami,K. |
| | | | Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Hayashida,K., Hayatsu,N., Hiramoto,K., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Ishii,Y., Itoh,M., Kagawa,J., Kanagawa,S., Katoch,H., Kawai,J., Kishikawa-Hirozane,T., Kohima,Y., Kondo,S., Konno,H., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sugabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku,Akira,S., Tanaka,T., Tomaru,A., Toyoda,T., Waki,K., Yasunishi,A. and Hayashizaki,Y. |
| | | FEATURES | Location/Qualifiers |
| | | source | 1..707 |
| | | | /organism="Oryza sativa (japonica cultivar-group)" |
| | | | /mol_type="mRNA" |
| | | | /organism="mRNA" |
| US-10-666-642-194_COPY_111_164 | (1-54) × AF426252 (1-585) | ACCESION | AK109578 |
| | | VERSION | AK109578.1 |
| | | DEFINITION | Oryza sativa (japonica cultivar-group) cDNA clone:002-135-F06, full insert sequence. |
| | | KEYWORD | G1:32994787 |
| | | SOURCE | FBI CDNA; Oligo capping. |
| | | ORGANISM | Oryza sativa (japonica cultivar-group) |
| | | REFERENCE | 1. Ehrhartoidae; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryzae; Oryza. |
| | | AUTHORS | The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kishimoto,N., Nakanishi,T., Nagata,T., Kawashima,N., Doi,K., Kojima,K., Nakanishi,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Tsunoda,Y., Kurokawa,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Kondo,S., Konno,H., Miyazaki,A., Ota,Y., Saitoh,R., Ishibiki,J., Kawamura,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:, Kawai,J., Carninci,P., Adachi,J., Aizawa,X., Arakawa,T., Shiraki,T., Hara,A., Hashidume,W., Hayatsu,N., Imotsu,K., Ishii,Y., Itoh,M., Kogawa,I., Kondo,S., Konno,H., Miyazaki,A., Ota,Y., Otsu,N., Ota,Y., Saitoh,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., YOSHINO, M. and Hayashizaki,Y. |
| | | TITLE | Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice |
| | | JOURNAL | Science 301 (5631), 376-379 (2003) |
| | | MEDLINE | 22752273 |
| | | PUBMED | 12869764 |
| | | REFERENCE | 2 (bases 1 to 707) |
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complement (17119 . 17559)

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CDS

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| Pred. No.: | Length: |
|------------------------|---------|
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| Score: | 24.00 |
| Percent Similarity: | 88.89% |
| Best Local Similarity: | 75.93% |
| Query Match: | 81.21% |
| DB: | 8 |
| Matches: | 41 |
| Conservative: | 7 |
| Mismatches: | 6 |
| Indels: | 0 |
| Gaps: | 0 |

US-10-666-642-194_COPY_111_164 (1-54) × AP002486 (1-149699)

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Qy 21 AsnTrtyrLtycysSerGlyLycysSerVallySlysLySargValGluLargAspGly 40
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RESULT 6

LOCUS AK108555

DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone: 002-144-E10, full insert sequence.

ACCESSION AK108555

VERSION AK108555.1 GI 32992764

KEYWORDS FLI CDNA; oligo capping.

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Poales; Poaceae;

Bhrhartooideae; Oryzeae; Oryza.

REFERENCE 1

| | |
|-------------------|---|
| AUTHORS | The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuka,K., Shishikiri,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Ocomo,Y., Murakami,K., Kurosoki,T., Sugano,Y., Fujimori,T., Suzuki,T., Tsunoda,Y., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikehara,R., Ishibiki,J., Kawamura,N., Mura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN, Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Harada,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yosino,H., and Hayashizaki,Y. |
| TITLE | Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice |
| JOURNAL | Science 301 (5631), 376-379 (2003) |
| MEDLINE PUBMED | 2272273 12869764 |
| REFERENCE AUTHORS | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashidume,W., Hayashizaki,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Horii,F., Hotta,I., Iida,J., Ieda,Y., Ikeda,R., Imamura,K., Tomoroni,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kishimoto,T., Kojima,Y., Kawai,J., Kawamura,M., Kanagawa,S., Katoh,H., Kawagashira,N., Kishimoto,T., Kohayashi,M., Kikuchi,S., Kishikawa,Hirozane,T., Kishimoto,N., Kohayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Konda,M., Koyaji,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Matsuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Numasaki,R., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Ohno,M., Ohneda,E., Ohno,M., Ohtsuka,K., Oka,M., Oita,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakagawa,A., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Sugiyama,A., Suzuki,K., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazziaki,J., Yokomizo,S., and Yoshimura,A. |
| COMMENT | This clone is one of the 28K full-length cDNA clones from japonica rice. Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel: +81-29-838-7007, Fax: +81-29-838-7007) |
| JOURNAL MEDLINE | 2272273 12869764 |

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|-------------------|---|
| AUTHORS | Ota,Y., Saitoh,H., Sakai,C., Sakazumi,N., Sano,H., Sasao,K., Satoh,K., Shiraki,T., Tagami,M., Tagami-Takeda,Y., Tagawa,Y., Tomaru,A., Toya,T., Waki,K., Yasunishi,A., and Hayashizaki,Y. |
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| REFERENCE AUTHORS | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashidume,W., Hayashizaki,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Horii,F., Hotta,I., Iida,J., Ieda,Y., Ikeda,R., Imamura,K., Tomoroni,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kishimoto,T., Kojima,Y., Kawai,J., Kawamura,M., Kanagawa,S., Katoh,H., Kawagashira,N., Kishimoto,T., Kohayashi,M., Kikuchi,S., Kishikawa,Hirozane,T., Kishimoto,N., Kohayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Konda,M., Koyaji,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Matsuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Numasaki,R., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Ohno,M., Ohneda,E., Ohno,M., Ohtsuka,K., Oka,M., Oita,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakagawa,A., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Sugiyama,A., Suzuki,K., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazziaki,J., Yokomizo,S., and Yoshimura,A. |
| COMMENT | Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel: +81-29-838-7007, Fax: +81-29-838-7007) |
| JOURNAL MEDLINE | 2272273 12869764 |

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|-------------------|---|
| AUTHORS | Ota,Y., Saitoh,H., Sakai,C., Sakazumi,N., Sano,H., Sasao,K., Satoh,K., Shiraki,T., Tagami,M., Tagami-Takeda,Y., Tagawa,Y., Tomaru,A., Toya,T., Waki,K., Yasunishi,A., and Hayashizaki,Y. |
| FEATURES SOURCE | Location/Qualifiers 1..1193 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nipponbare" /db_xref="taxon:39947" /clone="1002-144-B10" |
| ORIGIN | Alignment Scores: Pred. No.: 4.06e-22 Score: 237.00 Percent Similarity: 88.89% Best Local Similarity: 74.07% Query Match: 79.53% DB: 8 Length: 1193 Matches: 40 Conservative: 8 Mismatch: 6 Indels: 0 Gaps: 0 |
| REFERENCE AUTHORS | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashidume,W., Hayashizaki,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Horii,F., Hotta,I., Iida,J., Ieda,Y., Ikeda,R., Imamura,K., Tomoroni,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kishimoto,T., Kojima,Y., Kawai,J., Kawamura,M., Kanagawa,S., Katoh,H., Kawagashira,N., Kishimoto,T., Kohayashi,M., Kikuchi,S., Kishikawa,Hirozane,T., Kishimoto,N., Kohayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Konda,M., Koyaji,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Matsuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Numasaki,R., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Ohno,M., Ohneda,E., Ohno,M., Ohtsuka,K., Oka,M., Oita,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakagawa,A., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Sugiyama,A., Suzuki,K., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazziaki,J., Yokomizo,S., and Yoshimura,A. |
| COMMENT | Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel: +81-29-838-7007, Fax: +81-29-838-7007) |
| JOURNAL MEDLINE | 2272273 12869764 |

| | | | | | |
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| Db | 196 GATGGATAACGGGAGGTACGCCAAAACAGTAAGACAATCCATTCCCAAGG 255 | | Db | 197.00 Length: 548 Matches: 33 Conservative: 10 Mismatches: 11 Indels: 0 Gaps: 0 | |
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| Qy | 41 AspAspAlaAlaLysVallethrThrTrpGluGlyValHis 54 | | Qy | 21 AsnTrpTrpLysCysSerGluGlyCysSerValLysLysBargValGluArgAspGly 40 | |
| Db | 316 GGAGACGAAAGGAGCTGCTGTCAGCACATACACAGTGTTAT 357 | | Db | 279 AGCTTATAAGTGACAGAGGATCGAGCTGAAGCAGTCAGAACATCCACAG 338 | |
| RESULT 1.2 | | | Qy | 21 AspAspAlaAlaLysVallethrThrTrpGluGlyValHis 54 | |
| AY085246 | AY085246 548 bp mRNA linear PLN 14-APR-2003 | | Db | 41 AspAspAlaAlaLysVallethrThrTrpGluGlyValHis 54 | |
| LOCUS | AY085246 Arabidopsis thaliana clone 1415 mRNA, complete sequence. | | Db | 339 GGAGACGAAAGGAGCTGCTGTCAGCACATACACAGTGTTAT 380 | |
| DEFINITION | AY085246 | | Qy | AK118457 Atg01970 mRNA for putative WRKY-like transcriptional regulator protein, complete cds, clone: | |
| VERSION | AY085246.1 GI:21403956 | | Db | AK118457.1 GI:26451945 | |
| KEYWORDS | FLN CDNA. | | LOCUS | Arabidopsis thaliana Atg01970 mRNA for putative WRKY-like transcriptional regulator protein, complete cds, clone: | |
| SOURCE | Arabidopsis thaliana (thale cress) | | DEFINITION | Arabidopsis thaliana Atg01970 mRNA for putative WRKY-like transcriptional regulator protein, complete cds, clone: | |
| ORGANISM | Bacteriophage; Streptomyces; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. | | ACCESSION | AK118457 | |
| REFERENCE | Haas, B.J., Volkovskiy, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O., and Salzberg, S.L. | | VERSION | AK118457.1 GI:26451945 | |
| AUTHORS | Full-length messenger RNA sequences greatly improve genome annotation | | KEYWORDS | Arabidopsis thaliana (thale cress) | |
| JOURNAL | Genome Biol. 3 (6), RESEARCH0029 (2002) | | SOURCE | Arabidopsis thaliana | |
| MEDLINE | 22088475 | | ORGANISM | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. | |
| PUBMED | 12093376 | | REFERENCE | Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P., Kawai, J., Hayashizaki, Y., and Shinozaki, K. | |
| REFERENCES | 2 (bases 1 to 548) | | AUTHORS | Published Only in Database (2002) | |
| AUTHORS | Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K. | | TITLE | Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P., Kawai, J., Hayashizaki, Y., and Shinozaki, K. | |
| JOURNAL | Full-length cDNA from Arabidopsis thaliana | | JOURNAL | Direct Submission | |
| COMMENT | 3 (bases 1 to 548) | | REFERENCE | Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA | |
| JOURNAL | Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA | | AUTHORS | This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated, approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A | |
| JOURNAL | Submitted (25-NOV-2002) Motoaki Seti, RIKEN Genomic Sciences Center, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa | | TITLE | Submitted (25-NOV-2002) Motoaki Seti, RIKEN Genomic Sciences Center, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa | |
| JOURNAL | Submitted (1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa) | | JOURNAL | | |

Japan (E-mail: msekig@gsb.riken.go.jp,
URL: <http://pfeweb.gsb.riken.go.jp>, Tel: +81-45-503-9625,
Fax: +81-45-503-9986) Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al. (1998) Plant J. 15:707-720;
Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI
was ligated to modified Lambda FUC-1-E vector (Carninci et al. (2001) Genomics 77:79-90) digested with BamHI and Sali.
This clone is in a modified pBluescript vector.
Please visit our web site (<http://pfeweb.gsb.riken.go.jp/>) for
further details.

Location/Qualifiers

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ORIGIN

Search completed: August 26, 2005, 01:06:40
Job time: 2881 sec

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/lab host="E. coli"
/clone lib="Arabidopsis Leaf Senescence Library"
/note="Organ: Roette Leaf; Vector: pBluscript SKII+;
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and #6 (counted from the bottom) were harvested and
immediately frozen in liquid N2. The leaves were visibly
yellow excepted for the leaf base areas that were still
greenish."

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ORIGIN

| Alignment Scores: | | US-10-666-642-194_COPY_111_164 (1-54) x CDS29340 (1-435) | | | |
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| Score: | 1.13e-31 | Matches: | 54 | | |
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| Best Local Similarity: | 100.00% | Mismatches: | 0 | | |
| Query Match: | 100.00% | Indels: | 0 | | |
| DB: | 6 | Gaps: | 0 | | |

| RESULT 2 | | CB879380 (1-643) | | | |
|--------------|--|------------------|--|------|------------------------|
| RESULT | 2 | Length: | 643 bp | mRNA | linear EST 23-APR-2001 |
| LOCUS | CB879380 | DEFINITION | HP Hordeum vulgare subsp. vulgare cDNA clone HP11P20 | | |
| ORGANISM | Hordeum vulgare | 5'-PRIM., | | | |
| ACCESSION | CB879380 | 5-PRIM., | | | |
| VERSION | CB879380.1 | mRNA sequence. | | | |
| KEYWORDS | EST. | | | | |
| SOURCE | Zhang H., Wescle,W., Michalek,W., Stein,N. and Graner,A. | | | | |
| ORGANISM | Hordeum vulgare subsp. vulgare | | | | |
| EUKARYOTE | Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta; | | | | |
| SUPERKINGDOM | Spermato phyta; Magnoliophyta; Liliopsida; Poales; Poaceae; | | | | |
| PHYLUM | Pooidae; Triticeae; Hordeum. | | | | |
| CLASS | 1 (bases 1 to 643) | | | | |
| ORDER | Zhang H., Wescle,W., Michalek,W., Stein,N. and Graner,A. | | | | |
| GENUS | EST sequencing and analysis in barley (2002) | | | | |
| SPECIES | unpublished (2002) | | | | |
| REFERENCE | Contact: Stein, Nils | | | | |
| AUTHORS | Molecular Markers Group, Department Genbank | | | | |
| TITLE | Institute of Plant Genetics and Crop Plant Research (IPK) | | | | |
| JOURNAL | Corrensstr. 3, 06466, Gatersleben, Germany | | | | |
| COMMENT | Tel: 039482-55222 | | | | |
| FEATURES | Fax: 039482-55955 | | | | |
| source | Email: stein@ipk-gatersleben.de | | | | |
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| | Seq primer: T3. | | | | |
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    artefact present in the kit, in most cases the EcoRI site
    is NOT present, as well as the EcoRI adapter used for
    cloning. To excise the insert, restriction sites upstream
    of the vector should be used (e.g. BamHI, SalI, PstI). NOTE: Also
    due to the cloning system used Blue/white selection for
    recombinants is not 100% reliable. Average insert size is
    850 bp"

```

SITES: BCO RI (5'-end of cDNA) and Xba I (3'-end of cDNA).
NOTE: Due to a cloning artefact caused by the kit, in most

cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp"

ORIGIN

| | | | | | | | | |
|---|---|---------------|---|------------------------|--|---------------|--|--|
| Alignment Scores: | | | | | | | | |
| Pred. No.: | 4.4e-25 | Length: | 700 | | | | | |
| Score: | 253.00 | Matches: | 44 | | | | | |
| Percent Similarity: | 90.74% | Conservative: | 5 | | | | | |
| Best Local Similarity: | 81.48% | Mismatches: | 5 | | | | | |
| Query Match: | 84.90% | Indels: | 0 | | | | | |
| DB: | 1. | Gaps: | 0 | | | | | |
| US-10-666-642-194_COPY_111_164 (1-54) × AL503208 (1-700) | | | | | | | | |
| Qy | 1 AspGlyPheoyystPArgLystYrgLYLysSerVallysBarnylleAbySarg 20 | Qy | 1 AspGLYPhelystPArgLySystYrgLYLysSerVallysBarnylleAbySarg 20 | Score: | 253.00 | Matches: | 44 | |
| Db | 380 GACGGTACAGTCAGTGCCAGATGCCAGTAAGCTCGTCAAGAAGTCGGCAAG 439 | Db | 380 GACGGTACAGTCAGTGCCAGATGCCAGTAAGCTCGTCAAGAAGTCGGCAAG 439 | Percent Similarity: | 90.74% | Conservative: | 5 | |
| Qy | 21 AsntrytlylscysserSerGluGlycysSerVallysBargValGlyArgPgly 40 | Qy | 21 AsntrytlylscysserSerGluGlycysSerVallysBargValGlyArgPgly 40 | Best Local Similarity: | 81.48% | Mismatches: | 5 | |
| Db | 440 AACTACTACGGTCTCGAGGAGGGCAGCTGAGAGGAGGGCAGCTGAGAGG 499 | Db | 440 AACTACTACGGTCTCGAGGAGGGCAGCTGAGAGGAGGGCAGCTGAGAGG 499 | Query Match: | 84.90% | Indels: | 0 | |
| Qy | 41 AspAspAlaAlaLysValleThrThrThrGluGlyValHis 54 | Qy | 41 AspAspAlaAlaLysValleThrThrThrGluGlyValHis 54 | DB: | 1. | Gaps: | 0 | |
| Db | 500 GACGACCCGGGTACCTGGTACCGTGTACGGCACGGAC 541 | Db | 500 GACGACCCGGGTACCTGGTACCGTGTACGGCACGGAC 541 | RESULT 5 | | | | |
| Qy | 21 AsntrytlyrCysSerGluGlyCysSerVallysBargValGlyArgPgly 40 | Qy | 21 AsntrytlyrCysSerGluGlyCysSerVallysBargValGlyArgPgly 40 | LOCUS | BF009428 | LOCUS | BF009428 | |
| Db | 440 AACTACTACGGTCTCGAGGAGGGCAGCTGAGAGGAGGGCAGCG 499 | Db | 440 AACTACTACGGTCTCGAGGAGGGCAGCTGAGAGGAGGGCAGCG 499 | DEFINITION | BF009428 | DEFINITION | BF009428 | |
| Qy | 41 AspAspAlaAlaLysValleThrThrThrGluGlyValHis 54 | Qy | 41 AspAspAlaAlaLysValleThrThrThrGluGlyValHis 54 | ORGANISM | BF009428 | ORGANISM | BF009428 | |
| Db | 500 GACGACCCGGGTACCTGGTACCGTGTACGGCACGGAC 541 | Db | 500 GACGACCCGGGTACCTGGTACCGTGTACGGCACGGAC 541 | KEYWORDS | EST. | KEYWORDS | EST. | |
| RESULT 4 | | ORGANISM | Glycine max (soybean) | | | | | |
| BE412464 | BE412464 | LOCUS | Bacillus | | | | | |
| DEFINITION | MC0004_A09R900625 | VERSION | MC0004_A09R900625 | RELEASE | 1.0 | RELEASE | 1.0 | |
| ACCESSION | BE412464 | SOURCE | ITRC MCG Barley Leaf/Culm Library | ORGANISM | Tracheophyta; Streptophytina; Embryophytina; Tracheophyta; Fabaceae; Papilionoidea; Phaseoleae; Glycine. | REFERENCE | Shoemaker, R., Keim, P., Vodkin, L., Brelpelding, J., Coryell, V., Beck, C., Wylie, T., Marra, M., Hillier, L., Kucaba, T., Martin, J., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pope, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watsonson, R., and Wilson, R. | |
| VERSION | BE412464.1 | COMMENT | Unpublished ESTs: BU547499 corresponding to Gm-r1088-4620 (3') | COMMENT | Other ESTs: BU547499 corresponding to Gm-r1088-4620 (3') | COMMENT | Other ESTs: BU547499 corresponding to Gm-r1088-4620 (3') | |
| SOURCE | EST. | TITLE | Contact: Shoemaker R/ Public Soybean EST Project | JOURNAL | Public Soybean EST Project | JOURNAL | Public Soybean EST Project | |
| ORGANISM | Hordeum vulgare | KEYWORDS | Washington University School of Medicine | COMMENT | Washington University School of Medicine | COMMENT | Washington University School of Medicine | |
| Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Herrmann, P., Hermann, R.G., Holtom, T., Jacquin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Oghara, Y., Peccioni, N., Qualset, C., Schuch, W., Selvaraj, G., Sharifliou, M., Sorrells, M., Warburton, M., and Wenzel, G. | Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Herrmann, P., Hermann, R.G., Holtom, T., Jacquin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Oghara, Y., Peccioni, N., Qualset, C., Schuch, W., Selvaraj, G., Sharifliou, M., Sorrells, M., Warburton, M., and Wenzel, G. | FEATURES | International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae | FEATURES | International Triticeae EST Cooperative (ITEC) | FEATURES | International Triticeae EST Cooperative (ITEC) | |
| REVISION | BE412464.1 | COMMENT | Unpublished (2000) | COMMENT | Unpublished (1999) | COMMENT | Unpublished (1999) | |
| AUTHORS | GI:9410310 | COMMENT | Contact: estwatsen@wustl.edu | JOURNAL | Other ESTs: BU547499 corresponding to Gm-r1088-4620 (3') | JOURNAL | Other ESTs: BU547499 corresponding to Gm-r1088-4620 (3') | |
| VERSION | BE412464.1 | COMMENT | When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenomics Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) | JOURNAL | Public Soybean EST Project | JOURNAL | Public Soybean EST Project | |
| SOURCE | Hordeum vulgare | COMMENT | Insert Length: 1115 Std Error: 0.00 | JOURNAL | Washington University School of Medicine | JOURNAL | Washington University School of Medicine | |
| ORGANISM | Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum. | COMMENT | High quality sequence stop: 421. | JOURNAL | 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA | JOURNAL | 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA | |
| Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Herrmann, P., Hermann, R.G., Holtom, T., Jacquin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Oghara, Y., Peccioni, N., Qualset, C., Schuch, W., Selvaraj, G., Sharifliou, M., Sorrells, M., Warburton, M., and Wenzel, G. | Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Herrmann, P., Hermann, R.G., Holtom, T., Jacquin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Oghara, Y., Peccioni, N., Qualset, C., Schuch, W., Selvaraj, G., Sharifliou, M., Sorrells, M., Warburton, M., and Wenzel, G. | COMMENT | Tel: 314 286 1800 | JOURNAL | Tel: 314 286 1800 | JOURNAL | Tel: 314 286 1800 | |
| REVISION | BE412464.1 | COMMENT | Fax: 314 286 1810 | JOURNAL | Fax: 314 286 1810 | JOURNAL | Fax: 314 286 1810 | |
| AUTHORS | GI:9410310 | COMMENT | Location/Qualifiers | JOURNAL | Location/Qualifiers | JOURNAL | Location/Qualifiers | |
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| ORGANISM | Institute for Plant Genetics & Crop Plant Research Correnstr. 3, D-06466 Gatersleben GERMANY Tel: +49 39482 5521 Fax: +49 39482 5137 Email: a.graner@ipk-gatersleben.de International Triticeae EST Cooperative (ITEC) http://wheat.pw.usda.gov/genome/ | COMMENT | /mol_type="mRNA" | JOURNAL | /mol_type="mRNA" | JOURNAL | /mol_type="mRNA" | |
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| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |
| JOURNAL | | COMMENT | | JOURNAL | | JOURNAL | | |
| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |
| JOURNAL | | COMMENT | | JOURNAL | | JOURNAL | | |
| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |
| JOURNAL | | COMMENT | | JOURNAL | | JOURNAL | | |
| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |
| JOURNAL | | COMMENT | | JOURNAL | | JOURNAL | | |
| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |
| JOURNAL | | COMMENT | | JOURNAL | | JOURNAL | | |
| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |
| JOURNAL | | COMMENT | | JOURNAL | | JOURNAL | | |
| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |
| JOURNAL | | COMMENT | | JOURNAL | | JOURNAL | | |
| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |
| JOURNAL | | COMMENT | | JOURNAL | | JOURNAL | | |
| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |
| JOURNAL | | COMMENT | | JOURNAL | | JOURNAL | | |
| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |
| JOURNAL | | COMMENT | | JOURNAL | | JOURNAL | | |
| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |
| JOURNAL | | COMMENT | | JOURNAL | | JOURNAL | | |
| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |
| JOURNAL | | COMMENT | | JOURNAL | | JOURNAL | | |
| COMMENT | | COMMENT | | JOURNAL | | JOURNAL | | |
| FEATURES | source | COMMENT | | JOURNAL | | JOURNAL | | |

Page 4

chamber, excised above the soil level, and the plants prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XbaI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XbaI digestion. The cDNA fragments were directionally cloned into the EcoRI-XbaI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker.¹

RIGGIN

| Alignment Scores: | | US-10-666-642-194_COPY_111_164 (1-54) x BF009428 (1-549) | | | |
|---|-------------------|--|-------------|---------------|-------------------|
| Pred. | No.: | Length: | Matches: | Conservative: | Mismatches: |
| Score: | 8.67e-25 | 549 | 43 | 6 | 5 |
| Percent Similarity: | 250.00 | | | | |
| Best Local Similarity: | 90.74% | | | | |
| Query Match: | 79.63% | | | | |
| DB: | 83.89% | | | | |
| | 2 | Gaps: | 0 | | |
| RESULT 6 | | | | | |
| LOCUS | BUS47499 | 634 bp | mRNA | linear | EST 16-SEP-2002 |
| DEFINITION | GM88001320A06 | Gm-r1088 | Glycine max | CDNA clone | Gm-r1088-4620 3 , |
| VERSION | BUS47499 | GI:22930360 | | | |
| KEYWORDS | | | | | |
| SOURCE | | | | | |
| ORGANISM | | | | | |
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | | | | |
| Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; | | | | | |
| rosids; eurosids I; Fabales; Fabaceae; Palionoideae; Phaseoleae; | | | | | |
| Glycine. | | | | | |
| 1 (bases 1 to 634) | | | | | |
| Clough, S., Vodkin, L., Shoep, B., Strelomik, M., Schweitzer, P., Gong, G., Liu, L. | | | | | |
| Unpublished | | | | | |
| Other ESTs: BF009428 corresponding to Gm-c1064-248 (5') | | | | | |
| Comment: Contact: Vodkin, L.O., PI, A Functional Genomics Program for | | | | | |
| Soybean (NSF 9872565). | | | | | |
| Lewin, H. A. Director, Keck Center for Comparative and Functional | | | | | |
| Genomics | | | | | |
| University of Illinois | | | | | |
| Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA | | | | | |
| TEL: (217) 244-6147 | | | | | |
| FAX: (217) 333-4582 | | | | | |
| Email: l-vodkin@uiuc.edu | | | | | |
| Insert Length: 634 | | | | | |
| Plate: GM880013A20 | row: A column: 06 | | | | |
| Seq Primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3' | | | | | |
| High quality sequence stop: 634. | | | | | |
| Location/Qualifiers | | | | | |
| 1. .G34 | | | | | |
| /organism="Glycine max" | | | | | |
| FEATURES | | | | | |
| Source | | | | | |
| RESULT 7 | | | | | |
| BI209002 | | | | | |
| LOCUS | | | | | |
| DEFINITION | | | | | |
| RTNA sequence | | | | | |
| RTNA sequence | | | | | |

| | | | | | | | | |
|------------|---|-----|----------|--|--|--|--|--|
| VERSION | B1209002.1 | GI: | 14686726 | | | | | |
| KEYWORDS | Lycopersicon esculentum (tomato) | | | | | | | |
| SOURCE | Lycopersicon esculentum | | | | | | | |
| ORGANISM | Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. | | | | | | | |
| REFERENCE | (bases 1 to 671) | | | | | | | |
| AUTHORS | van der Hoeven,R., Sun,H., Bezzerezides,J., Cho,J., Utterback,R., Ronning,C. and Tanksley,S. | | | | | | | |
| TITLE | Generation of ESTs from Tomato Suspension Cultures | | | | | | | |
| JOURNAL | Unpublished (2001) | | | | | | | |
| COMMENT | Contact: CUGI | | | | | | | |
| FEATURES | source | | | | | | | |
| FEATURES | source | | | | | | | |
| FEATURES | source | | | | | | | |
| ORIGIN | | | | | | | | |
| ORIGIN | | | | | | | | |
| ORIGIN | | | | | | | | |
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| ORIGIN | | | | | | | | |
| RESULT | 9 | | | | | | | |
| LOCUS | BI433746 | | | | | | | |
| DEFINITION | EST36507 P. infestans-challenged potato leaf, compatible reaction | | | | | | | |
| ORGANISM | Solanum tuberosum cDNA clone PPCB103 5' | | | | | | | |
| KEYWORDS | EST. Solanaceae; Solanum; Solanum tuberosum (potato) | | | | | | | |
| RESULT | 8 | | | | | | | |
| LOCUS | BQ515840 | | | | | | | |
| DEFINITION | EST623255 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMIU36 3' end, mRNA sequence. | | | | | | | |
| ACCESSION | BQ515840 | | | | | | | |
| VERSION | BQ515840.1 | GI: | 21374709 | | | | | |
| SOURCE | Solanum tuberosum (potato) | | | | | | | |
| ORGANISM | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum. | | | | | | | |
| REFERENCE | Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A., Bougrini,O., Bueli,C.R., Ronning,C.M., Fry,W.E. and Baker,B. | | | | | | | |
| TITLE | Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction | | | | | | | |

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and http://genoplante.info.infobiogen.fr/.

FEATURES

| Source | Location/Qualifiers |
|---------|--|
| 1.. 466 | /organism="Zea mays" /mol_type="mRNA" /cullFivar="mixture" /db_xref="taxon:4577" /clone_lib="GenetAg2" |

ORIGIN

Alignment Scores:

Pred. No.: 9.83e-25 Score: 249.00 Length: 466

Percent Similarity: 88.89% Matches: 44
Best Local Similarity: 81.48% Conservative: 4
Query Match: 83.56% Mismatches: 6
DB: 6 Indels: 0
Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) × CD967539 (1-466)

Qy 1 AspGlyPhenylsTrArgLysTrGlyLysSerValLysAsnAsnIleAsnLysBarg 20
Db 11 GACGGATTCAAGTGGGAAGACTACCGAAAGGCCAAATCCACCG 70

Qy 21 AsnTyrTrPheLysCysSerSerGluGlyCysSerValLysBargValGluArgAspGly 40

Db 71 AACACTACCGCTGGCTGGTGGAGGGCTGGGGCTGGGTGAGAGGACCC 130

Qy 41 AspAspAlaAlaLysValLeThrThrTrGluGlyValHis 54
Db 131 GACGACCCCCCTACTCATCACACTAGACGCGTCAC 172

RESULT 12

AW744840 LOCUS AW744840_1 F02..91_A002 Light_Grown_1 mRNA linear EST 19-JUL-2000

DEFINITION Sequence_.
ACCESSION AW744840
VERSION 1
KEYWORDS EST
SOURCE Sorghum bicolor (orghum)
ORGANISM Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCD

REFERENCE 1 (bases 1 to 497)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt,L.H.
TITLE An EST database from Sorghum: ovaries of varying immature stages
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mppratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: T7
High quality sequence start: 45
High quality sequence stop: 497
POLYA=Yes

FEATURES Location/Qualifiers

1.. 497 /organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4578"
/clone_lib="Light_Grown_1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; site_1: Xhol; site_2:

ORIGIN

Alignment Scores:

ORIGIN

Alignment Scores:

<p

| | | | |
|--|---|---------------|-----|
| Pred. No.: | 1.07e-24 | Length: | 501 |
| Score: | 249.00 | Matches: | 44 |
| Percent Similarity: | 88.89% | Conservative: | 4 |
| Best Local Similarity: | 81.48% | Mismatches: | 6 |
| Query Match: | 83.56% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |
| US-10-666-642-194_COPY_111_164 (1-54) × BG049241 (1-501) | | | |
| Qy | 1 AspglyPhelystStrparglyStyrglyLysbysservallyBashAsnIleasnlysArg 20 | | |
| Db | 117 GATGGATTCAATGGAGGAAGTATGGAAACAGGGCTGAGAACGCCAAATCCAGG 176 | | |
| Qy | 21 AsntTyrTylsCysSerGluGlyCyservallylysArgvalGluArgaspGly 40 | | |
| Db | 177 AACTACTCGCCTGCTGCGAGGGCTGGCGGTAAAGAAGGAGGGACCGGC 236 | | |
| Qy | 41 AspAspAlaAlaTyrValleThrThrTyrGluGlyValHis 54 | | |
| Db | 237 GAGCACCCCGTAGCTCATCACCACTACAGCGGCTCRC 278 | | |
| RESULT 14 | | | |
| BE216050 | 584 bp mRNA linear EST 23-OCT-2001 | | |
| LOCUS | HV_CEB0009E04f Hordeum vulgare seedling green leaf EST library | | |
| DEFINITION | HV_CEB0009E005 (Blumeria challenged) Hordeum vulgare subsp. vulgare cDNA clone HV_CEB0009E04f, mRNA sequence. | | |
| ACCESSION | BE216050 | | |
| VERSION | BE216050.1 | | |
| KEYWORDS | GI:8903662 | | |
| SOURCE | Hordeum vulgare subsp. vulgare | | |
| ORGANISM | Hordeum vulgare subsp. vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; | | |
| REFERENCE | 1 (bases 1 to 584) | | |
| AUTHORS | Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D. | | |
| TITLE | Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla6) seedling leaf cDNA library unpublished (2001) | | |
| JOURNAL | Contact: Wing RA | | |
| COMMENT | Clemson University Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu | | |
| FEATURES | Total hg bases = 325 Seq. Primer: ATTAAACCCCTCACTAAAGGG High quality sequence stop: 556. Location/Qualifiers | | |
| Source | 1. -584 organism="Hordeum vulgare subsp. vulgare" mol_type="mRNA" /clone_id="CITI6151 (Mla6)" /sub_species="vulgare" /db_xref="HV_CEP0009E04f" /tissue_type="Seedling green leaf" /lab_host="SOUR" | | |
| | /clone_lib="Hordeum vulgare seedling green leaf EST" library_HVCDNA005 (Blumeria challenged)" /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: Xhol;" C.I. 16151 (Mla6) Plants were grown in the R Wise lab at Iowa State University Ames, IA 7 day old green seedlings were challenged with isolate 5874 (AvrMla6) of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the | | |
| RESULT 15 | | | |
| BM328984 | 610 bp mRNA linear EST 04-JAN-2002 | | |
| LOCUS | PIC1_31_H12_91_A002 Pathogen-infected compatible 1 (PIC1) Sorghum | | |
| DEFINITION | bicoFor cDNA, mRNA sequence. | | |
| ACCESSION | BM328984 | | |
| VERSION | BM328984.1 GI:18068121 | | |
| KEYWORDS | Sorghum bicolor (Sorghum) | | |
| ORGANISM | Sorghum bicolor Bikaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Sorghum. | | |
| REFERENCE | 1 (bases 1 to 610) | | |
| AUTHORS | Cordonnier-Pratt,M.-M., Gingole,A., Fang,G.C., Dean,R., Wing,R., Sudman,M. and Pratt,L.H. | | |
| TITLE | An EST database from Sorghum: plants infected with a compatible pathogen unpublished (2002) | | |
| JOURNAL | Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mpratt@uga.edu | | |
| COMMENT | Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or | | |

T7 sequencing primer, are presented as the reverse complement.

Seq primer: T7
High quality sequence start: 20
High quality sequence stop: 610

POLYA=Yes
FEATURES

Location/Qualifiers
source
1.
1..610
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="Bx623"
/db_xref="taxon:4558"
/tissue_type="Leaves"
/dev_stage="4-week-old seedlings infected with
Colletotrichum graminicola"
/clone_lib="Pathogen-infected compatible 1 (PIC1)"
/note="Vector: pBluescript II SK-
Site 1: XhoI; Site 2: EcoRI; Four-week-old sorghum
seedlings were sprayed with spore suspension prepared from
3-week-old PNM42I, a sorghum isolate of the anthracnose
pathogen Colletotrichum graminicola. Inoculated plants
were kept in a 25 C dark growth chamber with 100% relative
humidity for 24 hr, followed by 12/12 hr of light/dark
cycle at 25 C with 90% relative humidity for another 24
hr. All leaves were harvested and quick frozen with liquid
nitrogen and stored in a -80 C freezer. The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision.
WARNING: While most or all ESTs are expected to derive
from the host plant, no effort was made to eliminate ESTs
deriving from the pathogen."

ORIGIN

Alignment Scores:

| Pred. No.: | Length: |
|---|-----------------|
| Score: | 1.36e-24 |
| Percent Similarity: | 249.00 |
| Best Local Similarity: | 88.89% |
| Query Match: | 81.48% |
| DB: | 83.56% |
| | 4 |
| | 0 |
| US-10-666-642-194_COPY_111_164 (1..54) x BM328984 (1..610) | |
| Qy 1 AspGlyPhelystRtpargLysArgLysSerValLysAspAsnTleAsnLysArg 20 | Length: 610 |
| Db 133 GATGGATTCAATGGGAAGTATGGGAATCTGTCGAGGCTGGCTAGAAGCCTCAGTCAGGCTGTAGAACAGGCCATTCAAAG 192 | Matches: 44 |
| Qy 21 AsnTyTyLysCysSerSerLysArgValGluAspGly 40 | Conservative: 4 |
| Db 193 AACTACTACCCCTGCTCGAGGCTGGCTGAGGCTGGAGGACCC 252 | Mismatches: 6 |
| Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54 | Indels: 0 |
| Db 253 GAGGACCCCCCTACTCATCACACCTACGCGCGTCCAC 294 | Gaps: 0 |

Search completed: August 26, 2005, 01:46:02
Job time : 2312 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 25, 2005, 18:08:19 ; Search time 391 Seconds
(without alignments)

Title: US-10-666-642-194_COPY_111_164

Perfect score: 298

Sequence: 1 DGFKRNKYGKKSVRNNIKR. RVERDDAYVITYEGVH 54

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Dgapop 6.0 , Delext 7.0

Searched: 439206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Command line Parameters:

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-MOBL=Fframe+p2n,model -DEV=x14
-Q=fcgn2.1/USP01/SP001/US1066642/runat 25082005 1300052_24846/app/query.fasta_1.199
-DBN=Geneseq_16Dec04 -QPMI=Castap -SUFIX=tng -MINMATCH=0.1 -LOOpCL=0
-LOOPEXT=0 -UNITS=ubits -START=1 -END=-1 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MDB=LOCAL -OUTFM=pto -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US1066642 @CGN 1_1 644 @runat 25082005 1300052_24846 -NCPU=6 -ICPU=3
-NO MMAP -LARGEFILE=1 -SCORER=XS -SCORER=LOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELPOP=6 -DELEXT=7
```

Database : N_Geneseq_16Dec04:*

1: Geneseqm1980s:*

2: Geneseqn1990s:*

3: Geneseqn000s:*

4: Geneseqm2001as:*

5: Geneseqn2001bs:*

6: Geneseqn002as:*

7: Geneseqm2002bs:*

8: Geneseqn2003as:*

9: Geneseqn03bs:*

10: Geneseqm2003as:*

11: Geneseqn2003bs:*

12: Geneseqn004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-----------------|---------------------|
| 1 | 298 | 100.0 | 585 12 AD002392 | AD002392 Thalecres |
| 2 | 298 | 100.0 | 585 12 AD061726 | AD061726 Thalecres |
| 3 | 298 | 100.0 | 1917 3 AAC49725 | AAC49725 Arabidops |
| c 4 | 250 | 83.9 | 740 12 AD061551 | AD061551 Transcript |
| c 5 | 249 | 83.6 | 823 12 AD003201 | Corn orth |

ALIGNMENTS

RESULT 1

ID AD002392 standard; cDNA; 585 BP.
XX AD002392;
AC AD001672
XX DT 01-JUL-2004 (first entry)

Thalecress transcription factor cDNA #403.

Thalecress; transcription factor; ss; gene; plant; transgenic; abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress; phosphate limitation; potassium limitation; nitrogen limitation; hormone sensitivity; disease resistance; sugar sensing; seed germination; flowering; inflorescence architectural change; meristem cell differentiation; phyllotaxy; pical dominance; trichome development; seed development; premature senescence; delayed senescence; lethality; necrosis; plant size; leaf morphology; seed morphology; secondary metabolism; light response; shade avoidance.

Arabidopsis thaliana.

| OS | XX | XX | PN | US2004045049-A1. |
|----|----|----|----|------------------|
| | | | | |

PD 04-MAR-2004.

XX 10-APR-2003; 2003US-00412699.

XX PR 13-SEP-1999; 99US-00394519.

| | | |
|------------------------|--|--|
| XX | 18-SEP-2003; 2003W0-US030292. | 331 GATGGTTTAATGGAGGAAGTATGGCAAAGAAATTCTGTCAAAAACATAACAGAGG 390 |
| PP | | 21 AsnTrtyTrlyScsSerSerGluGlyCysSerValGluArgAspGly 40 |
| XX | 18-SEP-2002; 2002US-0411837P | 391 AATTACTAACATGCTCAAGTCAAGTGGGTTGCTCGTAGAGGGTAGAGGAGGTTGAG 450 |
| PR | 17-DEC-2002; 2002US-043166P | |
| PR | 24-APR-2003; 2003US-0465809P | |
| XX | (MENDL-) MENDEL BIOTECHNOLOGY INC. | |
| PA | Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL, Sherman BK; | |
| PI | Riechmann JL, Haake V, Dubell AN, Keddie JS, | |
| XX | WPI: 2004-330163/30. | |
| PT | New recombinant polynucleotide encoding transcription factor | |
| PT | polypeptides, useful for producing transgenic plants with advantageous | |
| PT | properties compared to a reference plant. | |
| XX | | |
| PS | Claim 1; SEQ ID NO 193; 510pp; English. | |
| CC | The present invention relates to novel Plant transcription factor proteins (I) and nucleotide sequences (II) (AD01534 AD063778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to osmotic stress, increased tolerance to cold, increased germination in cold, increased tolerance to heat, increased germination in heat, increased tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to disease, including fungal disease and particularly Botrytis, Fusarium and Botrytis, increased tolerance to multiple fungal pathogens, increased resistance to glycoside, increased sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ACC, altered sugar sensing, increased tolerance to sugars, altered carbon/nitrogen sensing, early flowering, late flowering, altered flower structure, loss of flower determinacy, reduced fertility, altered shoot meristem development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced apical dominance, altered trichome density, altered trichome development, altered trichome structure, altered root development, altered shade avoidance, altered seed ripening, altered seed germination, slow growth, fast growth, altered cell differentiation, altered cell proliferation, altered cell expansion, altered phase change, altered senescence, abnormal embryo development, altered programmed cell death, lethality when overexpressed, altered necrosis patterns, increased plant size, increased biomass, large seedlings, dwarfed plants, dark green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed coloration, altered seed size, altered seed shape, large seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seed prenyl content, altered leaf prenyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. | |
| CC | Sequence 585 BP; 202 A; 95 C; 135 G; 153 T; 0 U; 0 Other; | |
| SQ | Length: 585 Matches: 54 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 12 | |
| Alignment Scores: | | |
| Prec. No.: | 5.9e-34 | |
| Score: | 298.00 | |
| Percent Similarity: | 100.00% | |
| Best Local Similarity: | 100.00% | |
| Query Match: | 100.00% | |
| DB: | 0 | |
| XX | RESULT 3 AAC49725 ID AAC49725 standard; DNA; 1917 BP. XX | |
| XX | DT 18-OCT-2000 (first entry) | |
| XX | DB Arabidopsis thaliana DNA fragment SEQ ID NO: 62208. | |
| XX | KW Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; 88. | |
| XX | Arabidopsis thaliana. | |
| XX | PN EP1033405-A2. | |
| CC | XX | |
| CC | PD 06-SEP-2000. | |
| CC | XX | |
| CC | PR 25-FEB-2000; 2000EP-00301439. | |
| CC | XX | |
| CC | PR 25-FEB-1999; 990US-0121825P. | |
| CC | XX | |
| CC | PR 09-MAR-1999; 990US-0123180P. | |
| CC | XX | |
| CC | PR 09-MAR-1999; 990US-0123548P. | |
| CC | XX | |
| CC | PR 23-MAR-1999; 990US-0125788P. | |
| CC | XX | |
| CC | PR 25-MAR-1999; 990US-0126264P. | |
| CC | XX | |
| CC | PR 29-MAR-1999; 990US-0126785P. | |
| CC | XX | |
| CC | PR 01-APR-1999; 990US-0127462P. | |
| CC | XX | |
| CC | PR 06-APR-1999; 990US-0128234P. | |
| CC | XX | |
| CC | PR 08-APR-1999; 990US-0128714P. | |
| CC | XX | |
| CC | PR 16-APR-1999; 990US-0129845P. | |
| CC | XX | |
| CC | PR 19-APR-1999; 990US-0130077P. | |
| CC | XX | |
| CC | PR 21-APR-1999; 990US-0130449P. | |
| CC | XX | |
| CC | PR 23-APR-1999; 990US-0130510P. | |
| CC | XX | |
| CC | PR 28-APR-1999; 990US-0130894P. | |
| CC | XX | |
| CC | PR 30-APR-1999; 990US-0132048P. | |
| CC | XX | |
| CC | PR 04-MAY-1999; 990US-0132407P. | |
| CC | XX | |
| CC | PR 05-MAY-1999; 990US-0132484P. | |
| CC | XX | |
| CC | PR 06-MAY-1999; 990US-0132486P. | |
| CC | XX | |
| CC | PR 06-MAY-1999; 990US-0132487P. | |
| CC | XX | |
| CC | PR 07-MAY-1999; 990US-0132863P. | |
| CC | XX | |
| CC | PR 11-MAY-1999; 990US-0134256P. | |
| CC | XX | |
| CC | PR 14-MAY-1999; 990US-0134218P. | |
| CC | XX | |
| CC | PR 14-MAY-1999; 990US-0134219P. | |
| CC | XX | |
| CC | PR 20-MAY-1999; 990US-0135124P. | |
| CC | XX | |
| CC | PR 21-MAY-1999; 990US-0135353P. | |
| CC | XX | |
| CC | PR 24-MAY-1999; 990US-0135629P. | |
| CC | XX | |
| CC | PR 25-MAY-1999; 990US-0136021P. | |
| CC | XX | |
| CC | PR 27-MAY-1999; 990US-0136392P. | |
| CC | XX | |
| CC | PR 28-MAY-1999; 990US-0136782P. | |
| CC | XX | |
| CC | PR 01-JUN-1999; 990US-0137222P. | |
| CC | XX | |
| CC | PR 03-JUN-1999; 990US-0137528P. | |
| CC | XX | |
| CC | PR 04-JUN-1999; 990US-0137502P. | |
| CC | XX | |
| CC | PR 07-JUN-1999; 990US-0137724P. | |
| CC | XX | |
| CC | PR 08-JUN-1999; 990US-0138049P. | |
| CC | XX | |
| CC | PR 09-JUN-1999; 990US-0138540P. | |

US-10-666-642-194_COPY_111_164 (1-54) x AD01726 (1-585)

Qy 1 AspGlyPhylsTyrSArgLysTyrGlyLysLysSerValLysSAsnNleAsnLysBarg 20

| PR | 10-JUN-1999; | 99US-0138847P. | 9905-0148171P. |
|----|--------------|-----------------|--------------------------------|
| PR | 14-JUN-1999; | 99US-0139119P. | 9905-0148319P. |
| PR | 16-JUN-1999; | 99US-0139452P. | 9905-0148341P. |
| PR | 16-JUN-1999; | 99US-013953P. | 9905-0148565P. |
| PR | 17-JUN-1999; | 99US-0139492P. | 9905-0148684P. |
| PR | 18-JUN-1999; | 99US-0139454P. | 9905-0149368P. |
| PR | 18-JUN-1999; | 99US-0139460P. | 9905-0149902P. |
| PR | 18-JUN-1999; | 99US-0139455P. | 9905-0149175P. |
| PR | 18-JUN-1999; | 99US-0139456P. | 9905-0149426P. |
| PR | 18-JUN-1999; | 99US-0139457P. | 9905-0149722P. |
| PR | 18-JUN-1999; | 99US-0139458P. | 9905-0149723P. |
| PR | 18-JUN-1999; | 99US-0139459P. | 9905-0149929P. |
| PR | 18-JUN-1999; | 99US-0139460P. | 9905-0149919P. |
| PR | 18-JUN-1999; | 99US-0139462P. | 9905-0149919P. |
| PR | 18-JUN-1999; | 99US-0139463P. | 9905-0150566P. |
| PR | 18-JUN-1999; | 99US-0139463P. | 9905-0151065P. |
| PR | 18-JUN-1999; | 99US-0139466P. | 9905-0151066P. |
| PR | 21-JUN-1999; | 99US-0139417P. | 9905-0151180P. |
| PR | 22-JUN-1999; | 99US-0139461P. | 9905-0151303P. |
| PR | 23-JUN-1999; | 99US-0140153P. | 9905-0151438P. |
| PR | 01-JUL-1999; | 99US-0140354P. | 9905-0151930P. |
| PR | 02-JUL-1999; | 99US-0140959P. | 9905-0152363P. |
| PR | 06-JUL-1999; | 99US-0140823P. | 9905-0153070P. |
| PR | 29-JUN-1999; | 99US-0140911P. | 9905-0153758P. |
| PR | 30-JUN-1999; | 99US-0139899P. | 9905-0154018P. |
| PR | 01-JUL-1999; | 99US-0141842P. | 9905-0154039P. |
| PR | 01-JUL-1999; | 99US-0142154P. | 9905-0154779P. |
| PR | 02-JUL-1999; | 99US-0142055P. | 9905-0155139P. |
| PR | 06-JUL-1999; | 99US-0142390P. | 9905-0155486P. |
| PR | 08-JUL-1999; | 99US-0142803P. | 9905-0156459P. |
| PR | 09-JUL-1999; | 99US-0142220P. | 9905-0156458P. |
| PR | 12-JUL-1999; | 99US-0142977P. | 9905-0156596P. |
| PR | 13-JUL-1999; | 99US-014342P. | 9905-0157753P. |
| PR | 14-JUL-1999; | 99US-014324P. | 9905-0158294P. |
| PR | 15-JUL-1999; | 99US-0144005P. | 9905-0158295P. |
| PR | 16-JUL-1999; | 99US-0144085P. | 9905-0158295P. |
| PR | 16-JUL-1999; | 99US-0144086P. | 9905-0158232P. |
| PR | 19-JUL-1999; | 99US-0144325P. | 9905-0158369P. |
| PR | 19-JUL-1999; | 99US-0144331P. | 9905-0159294P. |
| PR | 19-JUL-1999; | 99US-0144332P. | 9905-0159638P. |
| PR | 19-JUL-1999; | 99US-0144333P. | 9905-0159584P. |
| PR | 19-JUL-1999; | 99US-0144334P. | 9905-0160741P. |
| PR | 19-JUL-1999; | 99US-0144335P. | 9905-0160767P. |
| PR | 20-JUL-1999; | 99US-0144352P. | 9905-0160768P. |
| PR | 20-JUL-1999; | 99US-0144432P. | 9905-0160770P. |
| PR | 20-JUL-1999; | 99US-01444884P. | 9905-0160814P. |
| PR | 21-JUL-1999; | 99US-0144814P. | 9905-0160815P. |
| PR | 21-JUL-1999; | 99US-0145086P. | 9905-01610980P. |
| PR | 21-JUL-1999; | 99US-0145088P. | 9905-0161360P. |
| PR | 22-JUL-1999; | 99US-0145085P. | 9905-0160989P. |
| PR | 22-JUL-1999; | 99US-0145216P. | 9905-0161404P. |
| PR | 22-JUL-1999; | 99US-0145087P. | 9905-0161405P. |
| PR | 22-JUL-1999; | 99US-0145089P. | 9905-0161406P. |
| PR | 22-JUL-1999; | 99US-0145192P. | 9905-0161359P. |
| PR | 23-JUL-1999; | 99US-0145145P. | 9905-0161360P. |
| PR | 23-JUL-1999; | 99US-0145218P. | 9905-0161360P. |
| PR | 23-JUL-1999; | 99US-0145224P. | 9905-0161361P. |
| PR | 26-JUL-1999; | 99US-0145216P. | 9905-0161920P. |
| PR | 27-JUL-1999; | 99US-0145193P. | 9905-0161992P. |
| PR | 27-JUL-1999; | 99US-0145198P. | 9905-0161993P. |
| PR | 27-JUL-1999; | 99US-0145199P. | 9905-0162142P. |
| PR | 04-AUG-1999; | 99US-014704P. | Alignment Scores: |
| PR | 05-AUG-1999; | 99US-0147102P. | Score: 2.84e-33 |
| PR | 05-AUG-1999; | 99US-0147192P. | Percent Similarity: 298.00 |
| PR | 06-AUG-1999; | 99US-014703P. | Best Local Similarity: 100.00% |
| PR | 06-AUG-1999; | 99US-014716P. | Query Match: 100.00% |

| | | |
|--|---|--|
| XX | 21 | AeNTYTYTLYcysSerSerGluGlyCysSerValLysArgValGluArgAspGly 40 |
| PP | 501 | AACTACTACCGCTCTCGAGGGCTGCCGTGAGAAGCCGTCGTGAGAAGCCG 560 |
| XX | | |
| PR | 18-SEP-2002; 2002US-0411837P | |
| PR | 17-DEC-2002; 2002US-0434166P | |
| PR | 24-APR-2003; 2003US-0465809P | |
| PA | (MENDL) MENDEL BIOTECHNOLOGY INC. | |
| XX | | |
| PI | Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL; Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK; | |
| PI | WPI; 2004-330163/30. | |
| XX | | |
| PT | New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant. | |
| PT | | |
| PT | | |
| XX | | |
| PS | Claim 1; SEQ ID NO 974; 510pp; English. | |
| XX | The present invention relates to novel Plant transcription factor proteins (I) and nucleotide sequences (II) (AD061534; AD063778). The sequences can be used to produce transgenic plants, which overexpress (III), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to osmotic stress, increased tolerance to cold, increased germination in heat, increased tolerance to heat, increased germination in cold, increased tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to disease, including fungal disease and particularly <i>Bryosiphon</i> , <i>Fusarium</i> and <i>Botrytis</i> , increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ACC, increased sensitivity to ACC, altered sugar sensing, increased tolerance to sugars, altered carbon/nitrogen sensing, early flowering, late flowering, altered flower structure, loss of flower determinacy, reduced fertility, altered shoot meristem development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced apical dominance, altered trichome density, altered trichome development, increased sensitivity to ACC, altered sugar sensing, increased tolerance to green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed coloration, altered seed size, altered seed shape, large seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seed prenyl content, altered leaf prenyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences . | |
| XX | | |
| Sequence | 823 BP; 172 A; 258 C; 247 G; 144 T; 0 U; 2 Other; | |
| SQ | | |
| Alignment Scores: | | |
| Pred. No.: | 1.42e-26 | Length: 823 |
| Score: | 249.00 | Matches: 44 |
| Percent Similarity: | 88.89% | Conservative: 4 |
| Best Local Similarity: | 81.48% | Mismatches: 6 |
| Query Match: | 83.56% | Indels: 0 |
| DB: | 12 | Gaps: 0 |
| US-10-666-642-194_COPY_111_164 (1-54) x AD062507 (1-823) | | |
| Qy | 21 | AeNTYTYTLYcysSerSerGluGlyCysSerValLysArgValGluAsnLeuAsnLeuAsn 20 |
| Db | 501 | AACTACTACCGCTCTCGAGGGCTGCCGTGAGAAGCCGTCGTGAGAAGCCG 560 |
| Qy | 41 | AePAspAlaLtyrVallethrthrTyrGluglyValHis 54 |
| Db | 561 | GACGACCCCCGTACCTACGTACCACTAGACGGGTCCAC 602 |
| RESULT 7 | | |
| ID | ADI43068 | standard; DNA: 1663 BP. |
| XX | | |
| AC | ADI43068; | |
| XX | | |
| DT | 22-APR-2004 (first entry) | |
| XX | | |
| DE | Plant transcription factor polynucleotide #1006. | |
| XX | | |
| KW | transgenic; plant; enhanced tolerance to abiotic stress; | |
| KW | glycophosphate tolerance; hormone sensitivity; disease resistance; | |
| KW | sugar sensing; flowering; flower structure; stem bifurcation; | |
| KW | branching pattern; apical dominance; trichome; stem morphology; | |
| KW | root growth; root hair; seed development; cell proliferation; | |
| KW | cell differentiation; premature senescence; necrosis; plant size; | |
| KW | leaf morphology; seed morphology; seed biochemistry; root anthocyanin; | |
| KW | plant anthocyanin; light response; shade avoidance; bioinformatic; | |
| KW | transcription factor; gene; ds. | |
| OS | Zea mays. | |
| XX | | |
| PN | US2004019927-A1. | |
| XX | | |
| PD | 29-JAN-2004. | |
| XX | | |
| PF | 25-FEB-2003; 2003US-00374780. | |
| XX | | |
| PR | 18-APR-2001; 2001US-00837944. | |
| XX | | |
| PA | (SHERMAN B K. (RIECHMANN J L. (JIAN) / JIANG C. (HEAR J. (HEAR J. / HEARD J B. (HAAK V. (HAAKE V. (CREE / CREELMAN R A. (RATC / RATCLIFFE O. (ADAM L J. (REUBER T L. (REUBER T L. (KEDDIE J. (BROWN P E. (PILG / PILGRIM M L. (DUBBL / DUBLIN A N. (PINB / PINEDA O. (YUG / YU G. | |
| XX | | |
| PA | Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V, Keddie J, Brown PE; | |
| PI | Creeelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Brown PE; | |
| PI | Pilgrim ML, Dubell AN, Pineda O, Yu G; | |
| XX | | |
| DR | WPI; 2004-132245/13. | |
| XX | | |
| PI | SEQ ID NO 1531; 435pp; English. | |
| XX | | |
| PT | New transgenic plant comprising a recombinant polynucleotide of any one | |
| PT | polynucleotide of any one of more than 500 nucleotide sequences fully | |
| PT | defined in the specification or its complement. The method of the | |
| PT | invention can be used to produce a plant having altered traits such as: | |
| PT | enhanced tolerance to abiotic stress; glycosphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; early or late flowering | |
| CC | The invention describes a transgenic plant comprising a recombinant | |
| CC | polynucleotide of any one of more than 500 nucleotide sequences fully | |
| CC | defined in the specification or its complement. The method of the | |
| CC | invention can be used to produce a plant having altered traits such as: | |
| CC | enhanced tolerance to abiotic stress; glycosphosphate tolerance; hormone | |
| CC | sensitivity; disease resistance; sugar sensing; early or late flowering | |
| Qy | 1 AspGlyPhylsystPArgLysTyrGlyLysLysSerValLysAsnAsnLeuAsnLeuAsn 20 | |
| DB | 441 GACGGATCAAGTGAGGAGTACCGCTGAGAACGGCTGAAGAACGCCAAATCCAAGG 500 | |

altered flower structure; change in stem bifurcations; altered branching pattern; reduced apical dominance; reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered trichome development; increase in trichome number; altered stem morphology; increased root growth; increased root hairs; altered seed development; altered cell proliferation or cell differentiation; rapid development; premature senescence; increased necrosis; increase in seedling or plant size; decreased plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant anthocyanins, or alteration in light response or shade avoidance. The transgenic plant, polynucleotides and polypeptides are useful in diagnostic methods. This sequence represents a plant bioinformatic search methods. This sequence represents an orthologue of *Arabidopsis thaliana* transcription factor, and an orthologue of *Arabidopsis thaliana* transcription factors isolated in the invention, that can be used in the creation of a transgenic plant with altered traits.

XX Sequence 1663 BP; 417 A; 453 C; 494 G; 299 T; 0 U; 0 Other;

SQ Alignment Scores:
 Pred. No.: 3.6e-26 Length: 1663
 Score: 249.00 Matches: 44
 Percent Similarity: 88.89% Conservative: 4
 Best Local Similarity: 81.48% Mismatches: 6
 Query Match: 83.56% Indels: 0
 DB: 12 Gaps: 0
 US-10-666-642-194_COPY_111_164 (1-54) x AD143068 (1-1663)
 Qy 1 AspGlyPhenylSerPheGlyLysSerVallysAsnIleAsnlysArg 20
 Db 1078 GRGGATTCACTGGGAAACTACGGGAAGGGCGTCAGAACGCCAATCCAAGC 1137
 Qy 21 AsnTYrTyrLysCysSerSerGluGlyCysSerVallysArgValGluArgAspGly 40
 Db 1138 AACTACTACCGTGCGTGGAGGCTGGCGGTGAAAGAGCGGTGGAGGGACCGC 1197
 Qy 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
 Db 1198 GAGGACCCCGTAGCTCATCCACCTACAGGGCTCAG 1239

RESULT 8
 ADO03208 DT 01-JUL-2004 (first entry)
 ID 2003US Standard; CDNA; 1663 BP.
 XX AC ADO03208;
 XX DT 01-JUL-2004 (first entry)

Corn orthologue of Thalecress transcription factor, cDNA #183.
 XX Corn transcription factor; ss; gene; plant; transgenic; abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress; phosphorus limitation; potassium limitation; nitrogen limitation; hormone sensitivity; disease resistance; sugar sensing; seed germination; flowering; inflorescence architectural change; meristem; cell differentiation; phyllotaxy; apical dominance; trichome development; seed development; premature senescence; delayed senescence; lethality; necrosis; plant size; leaf morphology; seed morphology; secondary metabolism; light response; shade avoidance. Zea mays.

PN US2004045049-A1.
 XX PD 04-MAR-2004.
 XX PP 10-APR-2003; 2003US-00412699.
 XX PR 13-SEP-1999; 99US-00394519.
 XX PR 21-JAN-2000; 2000US-0048976.
 XX PR 17-FEB-2000; 2000US-00505720.
 XX PR 22-MAR-2000; 2000US-00532391.
 XX PR 22-MAR-2000; 2000US-00533392.

PR 22-MAR-2000; 2000US-00533393.
 PR 06-APR-2000; 2000US-00533648.
 PR 16-NOV-2000; 2000WO-US009448.
 PR 27-MAR-2001; 2001US-00819142.
 PR 17-APR-2001; 2001US-00837444.
 PR 30-APR-2002; 2002US-00958131.
 PR 14-JUN-2002; 2002US-00171468.
 PR 09-AUG-2002; 2002US-00225066.
 PR 09-AUG-2002; 2002US-00225067.
 PR 09-AUG-2002; 2002US-00225068.
 PR 17-DEC-2002; 2002US-0431166P.
 PR 25-FEB-2003; 2003US-00374780.

XX PA (ZHAN/) ZHANG J.
 PA (ZHAN/) FROMM M. E.
 PA (HEAR/) HEARD J. E.
 PA (RIEG/) RIECHMANN J. L.
 PA (ADAM/) ADAM L. J.
 PA (BROU/) BROU P. E.
 PA (PINE/) PINEDA O.
 PA (REUB/) REUBER T. L.
 PA (KEDDIE/) KEDDIE J. S.
 PA (YU G.) YU G.
 PA (JIANG/) JIANG C.
 PA (SAMAH/) SAMAH R. S.
 PA (PILG/) PILGRIM M. L.
 PA (CREE/) CREELMAN R. A.
 PA (DUBE/) DUBELL A. N.
 PA (RATC/) RATCLIFFE O.
 PA (KUMIMO/) KUMIMOTO R.
 PA (SHER/) SHERMAN B. K.
 WPI; 2004-225755/21.

XX PR New transgenic plant, useful in developing phenotypes with altered or improved characteristics or traits.

XX PA Claim 1; SEQ ID NO 1622; 213pp; English.

XX PA New transgenic plant, useful in developing phenotypes with altered or improved characteristics or traits.

XX PA Claim 1; SEQ ID NO 1622; 213pp; English.

XX CC The invention relates to a transgenic plant comprises a recombinant polynucleotide having a polynucleotide sequence or its complementary sequence comprising a sequence encoding a polypeptide, that initiates transcription (i.e. a transcription factor) from *Arabidopsis*, *Soybean*, *Rice*, *Rape* or *Corn*, comprising any of the sequences appearing as ADO01588 -ADO03527 or ADO0330-ADO0359. Also included are using a transgenic plant to grow a progeny plant, an expression cassette (comprising a constitutive, inducible or tissue-specific promoter and a recombinant polynucleotide described above), a host cell comprising the expression cassette, producing a modified plant having a modified trait, identifying a factor that is modulated by or interacts with a polypeptide encoded by the polynucleotide sequence and identifying at least one downstream polypeptide sequence that is subject to a regulatory effect of any of the polypeptides encoded by the polynucleotide described above. The transgenic plant is useful for producing a plant that has an altered trait, e.g. an enhanced tolerance to abiotic stress (increased tolerance to heat, tolerance to drought, tolerance to osmotic stress, tolerance to salt, tolerance to phosphate limitation, tolerance to potassium limitation, decreased sensitivity to nitrogen limitation), altered hormone sensitivity, reduced sensitivity to abscisic acid, an altered response to ethylene, disease resistance, altered susceptibility to *Botrytis*, altered susceptibility to *Fusarium*, altered susceptibility to *Bryophyce*, altered susceptibility to *Pseudomonas syringae*, altered susceptibility to *Sclerotinia*, altered sugar sensing, improved seed germination and seedling vigor, early flowering, late flowering, extended period of flowering, an inflorescence architectural change, a change in

stem bifurcations, a lack of a shoot meristem, reduced meristem cell differentiation, altered phyllotaxy, altered branching pattern, reduced apical dominance, reduced trichome density, ectopic trichome development, altered trichome morphology, increased root growth, increased root hairs, altered root development, altered cell proliferation/cell differentiation, premature senescence, delayed senescence, lethality, increased necrosis, an increase in seedling or plant size, decreased plant size, a change in leaf morphology, increased altered leaf development, increased leaf size and mass, glossy leaves, leaf cell expansion, change in seed morphology, altered seed coloration, increased seed size, decreased seed shape, change in leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid content, increased leaf insoluble sugars, decreased leaf insoluble sugars, increased leaf anthocyanins, an alteration of leaf fatty acid content, an alteration of leaf Glucosinolate content, change in seed oil biochemistry, an increase in seed oil content, decrease in seed fatty acid content, increase in seed fatty acid content, decrease in seed protein content, increase in seed protein content, decrease in seed protein content, alteration in seed prenyl lipid content, increase in seed sterols, upregulation of genes involved in secondary metabolism, increase in root anthocyanins, increase in plant anthocyanins, and alteration in light response or shade avoidance. The present sequence encodes an orthologue of a thalecress transcription factor isolated from Corn.

Sequence 1663 BP; 417 A; 453 C; 494 G; 299 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|---|---|---------------|------|
| Pred. No. : | 3.6e-26 | Length: | 1663 |
| Score: | 249.00 | Matches: | 44 |
| Percent Similarity: | 88.89% | Conservative: | 4 |
| Best Local Similarity: | 81.48% | Mismatches: | 6 |
| Query Match: | 83.56% | Indels: | 0 |
| DB: | 12 | Gaps: | 0 |
| US-10-666-642-194_COPY_111_164 (1-54) x ADO03208 (1-1663) | | | |
| Qy | 1 AspGlyPhenylsTrArgLysTrLysLysSerValLysAsnBnLleAsnBnLysArg 20 | | |
| Db | 1078 GACGGATTCAAGTGGAGGAGTACCGGAAGAGGGCTGAGACAGGCCAAATCCAGG 1137 | | |
| Qy | 21 AsnTyrTyrosCysSerSerGluLysCysSerValLysLysArgValGluArgAspGly 40 | | |
| Db | 1138 AACACTACCTGCTGCGAGGCGCTGGCGTGAAAGAACGGCGTGTGAGAGGGACCC 1197 | | |
| Qy | 41 AspAPAPAlaLysValLeuThrThrYglGluValHis 54 | | |
| Db | 1198 GACGACCCCCGCTACSTCATCACCCACCTAGCGCGTCCAC 1239 | | |

RESULT 9
ID ADO03200 standard; cDNA; 680 BP.

XX AC ADO03200;

XX DT 01-JUL-2004 (first entry)

Corn orthologue of Thalecress transcription factor, cDNA #179.

Corn: transcription factor; ss; gene; plant; transgenic; abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress; phosphate limitation; potassium limitation; nitrogen limitation; hormone sensitivity; disease resistance; sugar sensing; seed germination; flowering; inflorescence architectural change; meristem cell differentiation; phyllotaxy; apical dominance; trichome development; seed development; premature senescence; delayed senescence; lethality; necrosis; plant size; leaf morphology; seed morphology; secondary metabolism; light response; shade avoidance. Zea mays.
 XX PN US2004045049-A1.
 XX PD 04-MAR-2004.

XX PR 10-APR-2003; 2003US-00412699.
 XX PR 13-SEP-1999; 99US-00394519.
 PR 21-JAN-2000; 2000US-00489376.
 PR 17-FEB-2000; 2000US-00506720.
 PR 22-MAR-2000; 2000US-00532591.
 PR 22-MAR-2000; 2000US-00533029.
 PR 22-MAR-2000; 2000US-00533030.
 PR 22-MAR-2000; 2000US-00533392.
 PR 22-MAR-2000; 2000US-00533648.
 PR 06-APR-2000; 2000US-00509448.
 PR 16-NOV-2000; 2000US-00713994.
 PR 27-MAR-2001; 2001US-00819142.
 PR 17-APR-2001; 2001US-00837442.
 PR 30-JAN-2002; 2002US-00958131.
 PR 14-JUN-2002; 2002US-00171468.
 PR 09-AUG-2002; 2002US-00225066.
 PR 09-AUG-2002; 2002US-00225067.
 PR 09-AUG-2002; 2002US-00225068.
 PR 17-DEC-2002; 2002US-0034166P.
 PR 25-FEB-2003; 2003US-00374780.

XX PA (ZHAN/) ZHANG J.
 PA (ZHAN/) FROMM M. E.
 PA (HEAR/ J. E.
 PA (RIEC/ RIECHMANN J. L.
 PA (ADAM/ ADAM L. J.
 PA (BROU/ BROUN P. E.
 PA (PIN/ PINEDA O.
 PA (REUB/ REUBER T. L.
 PA (KEDDIE/ KEDDIE J. S.
 PA (YOGG/ YU G.
 PA (JIAN/ JIANG C.
 PA (SAM/ SAMARA R. S.
 PA (PILG/ PILGRIM M. L.
 PA (CREB/ CREELMAN R. A.
 PA (DUBE/ DUBELL A. N.
 PA (RATIC/ RATCLIFFE O.
 PA (KUM/ KUMIMOTO R.
 PA (SHER/ SHERMAN B. K.
 XX PI Zhang J., Fromm MB., Heard JB., Riechmann JL., Adam LJ., Broun PE.;
 PI Pineda O., Reuber TL., Keddie JS., Yu G., Jiang C., Samaha RS.;
 PI Pilgrim ML., Creelman RA., Dubell AN., Ratcliffe O., Kumimoto R.;
 PI Sherman BK;
 XX DR WPI; 2004-22575/21.

XX PT New transgenic plant, useful in developing phenotypes with altered or improved characteristics or traits.

XX PT Claim 1; SEQ ID NO 1614; 213pp; English.

XX PS XX

CC The invention relates to a transgenic plant comprising a recombinant polynucleotide having a polynucleotide sequence or its complementary sequence comprising a sequence encoding a polypeptide, that initiates transcription (i.e. a transcription factor) from *Arabidopsis*, *Soybean*, *Rice*, *Rape* or *Corn*, comprising any of the sequences appearing as ADO01588 -ADO15527 or ADO031530-ADO0559. Also included are using a transgenic plant to grow a progeny plant, an expression cassette (comprising a constitutive, inducible or tissue-specific promoter and a recombinant polynucleotide described above), a host cell comprising the expression cassette, producing a modified plant having a modified trait, identifying a factor that is modulated by or interacts with a polypeptide encoded by the polynucleotide sequence and identifying at least one downstream polynucleotide sequence that is subject to a regulatory effect of any of the polypeptides encoded by the polynucleotide described above. The transgenic plant is useful for producing a plant that has an altered trait e.g. an enhanced tolerance to abiotic stress (increased tolerance to chilling, germination in cold conditions, freezing tolerance, tolerance to heat, tolerance to drought, tolerance to osmotic stress, tolerance to salt, tolerance to phosphate limitation, tolerance to potassium

| | | | |
|-----------|-------------|--|---|
| Y | 1 | AasGlyPhelYstTrpArgLysTrpGlyLysAlaSerValLysAspAsnIleAsnYsAsg 20 | |
| b | 57 | GACGGCTAACAGTGAGGAAGTACGCCAAAGACTCCCTCARGAACTAGCCCCRAACCAAGG 116 | |
| Y | 21 | AsnTyrTyrLysCysSerLysGlyCysSerValLysArgValGluArgAspGly 40 | |
| b | 117 | AACTACTACCGGTGTCGACGGAAAGGTGCACTGAACTGAAAGGGTTGGGGCAAG 176 | |
| Y | 41 | AspAspAlaLysValIleThrThrTrpGlyValHis 54 | |
| b | 177 | GACGACCCAGCTTAATGGTGACGACCTACAGGGATGAC 218 | |
| RESULT 11 | | | |
| | AD003199 | standard; cDNA; 743 BP. | |
| D | AD003199 | | |
| X | AD003199; | | |
| C | | | |
| T | | | (first entry) |
| T | 01-JUL-2004 | | |
| X | | | Corn orthologue of Thalecress transcription factor, cDNA #178. |
| X | | | |
| X | | | Corn; transcription factor; ss; gene; plant; transgenic; abiotic stress; |
| X | | | cold tolerance; heat tolerance; drought; osmotic stress; |
| X | | | phosphate limitation; potassium limitation; nitrogen limitation; |
| X | | | hormone sensitivity; disease resistance; sugar sensing; seed germination; |
| X | | | flowering; inflorescence architectural change; |
| X | | | meristem cell differentiation; phyllotaxy; apical dominance; |
| X | | | trichome development; seed development; premature senescence; |
| X | | | delayed senescence; lethality; necrosis; plant size; leaf morphology; |
| X | | | seed morphology; secondary metabolism; light response; shade avoidance. |
| X | | | Zea mays |

X X US2004045049-A1.
 X X
 X X 04-MAR-2004.
 X X
 X X 10-APR-2003; 2003US-00412699.
 X X
 X X 13-SEP-1999; 99US-00394519.
 X X 21-JAN-2000; 2000US-00489376.
 X X 17-FEB-2000; 2000US-00506720.
 X X 22-MAR-2000; 2000US-00532591.
 X X 22-MAR-2000; 2000US-00533029.
 X X 22-MAR-2000; 2000US-00533030.
 X X 22-MAR-2000; 2000US-00533392.
 X X 22-MAR-2000; 2000US-00533648.
 X X 06-APR-2000; 2000WO-US009448.
 X X 16-NOV-2000; 2000US-00713394.
 X X 27-MAR-2001; 2001US-00819142.
 X X 17-APR-2001; 2001US-00817444.
 X X 30-JAN-2002; 2002US-00958131.
 X X 14-JUN-2002; 2002US-00171468.
 X X 09-AUG-2004; 2002US-00225066.
 X X 09-AUG-2002; 2002US-00225067.
 X X 09-AUG-2002; 2002US-00225068.
 X X 17-DRS-2002; 2002US-0434166P.

25-FEB-2003; 2003US-00374780.
CC sugars, increased leaf anthocyanin, an alteration of leaf fatty acid
CC content, an alteration of leaf Glucosinolate content, change in seed
CC biochemistry, an increase in seed oil content, decrease in seed fatty acid
CC content, increase in seed protein content, decrease in seed protein
CC content, alteration in seed prenyl lipid content, increase in seed
CC sterols, upregulation of genes involved in secondary metabolism, increase
CC in root anthocyanins, increase in Plant anthocyanins, and alteration in
CC light response or shade avoidance. The present sequence encodes an
CC orthologome of a thalecress transcription factor isolated from Corn.

Score: 248.00
 Percent Similarity: 92.59%
 Best Local Similarity: 77.78%
 Query Match: 83.22%
 DB: 12

US-10-666-642-194_COPY_111_164 (1-54) x ADO03199 (1-743)

Qy 1 AspGlyPhenylTrpArgLysTrgLysBlySerValLysAsnTleAsnTysArg 20
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:
 db 18 GAGGGTACAACTGGGAAATGACGCCCTAAGACGCCAACCAAGG 77

Qy 21 AsnTYrTyLysCysSerGluGlyCysSerValLysArgValGluArgAspGly 40
 |||||:|||||:|||||:|||||:|||||:|||||:
 db 78 ACTACTAACCGCTGCTGAAGGTGACGTGAGAGGGGTTGGAGGGACAAG 137

Qy 41 AspAspAlaAlaTyrValIleThrThrGluGlyValHis 54
 |||||:|||||:|||||:|||||:|||||:
 db 138 GACGACCCCAAGCTTACGTGTTGACGACTACAGGGATGCA 179

RESULT 12
 ADO62505
 ID ADO62505 standard; DNA; 743 BP.
 XX
 AC ADO62505;
 XX DT 15-JUL-2004 (First entry)
 XX DE Transcription factor G1274 orthologous sequence, SEQ ID 972.
 XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;
 KW osmotic stress tolerance; cold tolerance; heat tolerance;
 KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
 KW glyphosate resistance; flowering; fertility; seed development; ds.
 XX zea mays.
 XX WO2004031349-A2.
 XX PN 15-APR-2004.
 XX PD 18-SEP-2003; 2003WO-US0303292.
 XX PR 18-SEP-2002; 2002US-0411837P.
 XX PR 17-DEC-2002; 2002US-0434166P.
 XX PR 24-APR-2003; 2003US-0465809P.
 XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.

Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL,
 Riechmann JL, Haake V, Dubell AN, Keddie JS,
 WPI; 2004-330163/30.

XX New recombinant polynucleotide encoding transcription factor
 PT polypeptides, useful for producing transgenic plants with advantageous
 PT properties compared to a reference plant.
 XX Claim 1; SEQ ID NO 972; 510pp; English.

XX The present invention relates to novel plant transcription factor
 CC proteins (I) and nucleotide sequences (II) (ADO6134-ADO63778). The
 CC sequences can be used to produce transgenic plants, which overexpress
 CC (II), where the transgenic plant has an altered trait as compared to a
 CC non-transgenic plant or wild-type plant. The transgenic plant comprises
 CC an altered trait selected from increased tolerance to abiotic stress,
 CC increased tolerance to osmotic stress, increased tolerance to cold,
 CC increased germination in cold, increased tolerance to heat, increased
 CC increased tolerance to freezing conditions, increased tolerance to
 CC low nitrogen conditions, increased tolerance to disease, including
 CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,
 CC increased tolerance to multiple fungal pathogens, increased resistance to

Score: 42
 Conservative: 8
 Mismatches: 1
 Indels: 0
 Gaps: 0

CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
 CC increased sensitivity to ACC, altered sugar sensing, increased tolerance
 CC to sugars, altered carbon/nitrogen sensing, early flowering, late
 CC flowering, altered flower structure, loss of flower determinacy, reduced
 CC fertility, altered shoot meristem development, altered branching pattern,
 CC altered stem morphology, altered vascular tissue structure, reduced
 CC apical dominance, altered trichome density, altered cistema development,
 CC altered trichome structure, altered root development, altered shade
 CC avoidance, altered seed development, altered seed ripening, altered seed
 germination, slow growth, altered cell differentiation, altered cell
 CC proliferation, altered cell expansion, altered phase change,
 CC altered senescence, abnormal embryo development, altered programmed cell
 death, lethality when over-expressed, altered necrosis patterns, increased
 CC plant size, increased biomass, large seedlings, dwarfed plants, dark
 green leaves, change in leaf shape, increased leaf size and mass, light
 green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
 CC altered seed coloration, altered seed size, altered seed shape, large
 seed, increased leaf wax, increased leaf fatty acids, altered seed oil
 content, altered seed protein content, altered seed prey oil content,
 CC altered leaf prey lipid content, increased anthocyanin levels, and
 CC decreased anthocyanin levels. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 743 BP; 158 A; 210 C; 216 G; 159 T; 0 U; 0 Other;

Alignment Scores:
 DE Pred. No.: 1 1.73e-26
 Score: 248.00 Length: 743
 Percent Similarity: 92.59% Matches: 42
 Best Local Similarity: 77.78% Conservative: 8
 Query Match: 83.22% Mismatches: 4
 DB: 12 Indexes: 0
 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x ADO62505 (1-743)

Qy 1 AspGlyPhenylTrpArgLysTrgLysBlySerValLysAsnTysArg 20
 |||||:|||||:|||||:|||||:|||||:
 Db 18 GACGGCTACAGTGGAAAGTACGGCAAGAACGTCAGACAGGCCAACCAAGG 77

Qy 21 AsnTYrTyLysCysSerGluGlyCysSerValLysArgValGluArgAspGly 40
 |||||:|||||:|||||:|||||:
 Db 78 AACATACCCGGTGCCTGAGCTACGGTGTGACGACTACAGGTGCAACGTGAGGCGTGCACGGGACAAG 137

Qy 41 AspAspAlaAlaTyrValIleThrThrGluGlyValHis 54
 |||||:|||||:|||||:
 Db 138 GACGACCCAGCTACGGTACGGTACGGGATGAC 179

RESULT 13
 ADO03196/c
 ID ADO03196 standard; CDNA; 974 BP.
 XX AC ADO03196;
 XX DT 01-JUL-2004 (First entry)
 XX Soybean orthologue of Thalecress transcription factor, CDNA #267.

DE XX
 KW soybean; transcription factor; ss; gene; plant; transgenic;
 KW abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress;
 KW phosphate limitation; potassium limitation; nitrogen limitation;
 KW hormone sensitivity; disease resistance; sugar sensing; seed germination;
 KW flowering; inflorescence architecture change;
 KW meristem cell differentiation; phyllotaxy; apical dominance;
 KW trichome development; seed development; premature senescence;
 KW delayed senescence; lethality; necrosis; plant size; leaf morphology;
 KW seed morphology; secondary metabolism; light response; shade avoidance.
 XX OS Glycine max.
 XX
 PN US2004045049-A1.
 XX
 PN US2004045049-A1.

PD 04-MAR-2004.
 XX
 PF 10-APR-2003; 2003US-00412699.
 XX
 PR 13-SEP-1999; 99US-00394519.
 PR 21-JAN-2000; 2000US-00489376.
 PR 17-FEB-2000; 2000US-00506720.
 PR 22-MAR-2000; 2000US-00532591.
 PR 22-MAR-2000; 2000US-00531029.
 PR 22-MAR-2000; 2000US-00531030.
 PR 22-MAR-2000; 2000US-00531392.
 PR 22-MAR-2000; 2000US-00531648.
 PR 06-APR-2000; 2000WO-US009448.
 PR 16-NOV-2000; 2000US-00713994.
 PR 27-MAR-2001; 2001US-00819142.
 PR 17-AER-2001; 2001US-00837444.
 PR 30-JAN-2002; 2002US-00958131.
 PR 14-JUN-2002; 2002US-00171468.
 PR 09-AUG-2002; 2002US-0025066.
 PR 09-AUG-2002; 2002US-00225067.
 PR 09-AUG-2002; 2002US-00225068.
 PR 17-DEC-2002; 2002US-0434166P.
 PR 25-FEB-2003; 2003US-00374780.
 XX
 PA (ZHAN/) ZHANG J.
 PA (FROM/) FROMM M E.
 PA (HEAR/) HEARD J E.
 PA (RIECH/) RIECHMANN J L.
 PA (ADAM/) ADAM L J.
 PA (BROU/) BROUN P B.
 PA (PINE/) PINEDA O.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J S.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAM/) SAMAH R S.
 PA (PILG/) PILGRIM M L.
 PA (CREE/) CREELMAN R A.
 PA (DUBE/) DUBELL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KUMI/) KUMIMOTO R.
 PA (SHER/) SHERMAN B K.
 XX
 PI Zhang J., Heard J S., Riechmann JL., Adam LJ., Broun PB.;
 PI Pineda O., Reuber TL., Keddie JS., Yu G., Jiang C., Samaha RS.;
 PI Pilgrim ML., Creelman RA., Dubell AN., Ratcliffe O., Kumimoto R.;
 PI Sherman BK;
 XX
 DR 2004-225755/21.
 PT New transgenic plant, useful in developing phenotypes with altered or improved characteristics or traits.
 PS Claim 1; SEQ ID NO 1610; 213pp; English.
 XX
 CC The invention relates to a transgenic plant comprising a recombinant polynucleotide having a polynucleotide sequence or its complementary sequence comprising a sequence encoding a polypeptide, that initiates transcription (i.e. a transcription factor) from Arabidopsis, Soybean, Rice, Rape or Corn, comprising any of the sequences appearing as AD001588 -AD03527 or AD003530-AD03559. Also included are using a transgenic plant to grow a progeny plant, an expression cassette (comprising a constitutive, inducible or tissue-specific promoter and a recombinant polynucleotide described above), a host cell comprising the expression cassette, producing a modified plant having a modified trait, identifying a factor that is modulated by or interacts with a polypeptide encoded by the polynucleotide sequence and subject to a regulatory effect of any of the polypeptides encoded by the polynucleotide described above. The transgenic plant is useful for producing a plant that has an altered trait e.g. an enhanced tolerance to abiotic stress (increased tolerance to chilling, germination in cold conditions, freezing tolerance, tolerance to heat, tolerance to drought, tolerance to osmotic stress, tolerance to

CC salt, tolerance to phosphate limitation, tolerance to potassium limitation, decreased sensitivity to nitrogen limitation), altered hormone sensitivity, reduced sensitivity to abscisic acid, an altered response to ethylene, disease resistance, altered susceptibility to Botrytis, altered susceptibility to Fusarium, altered susceptibility to Erysiphe, altered susceptibility to Pseudomonas syringae, altered susceptibility to Sclerotinia, altered sugar sensing, improved seed germination and seedling vigor, early flowering, late flowering, extended period of flowering, an inflorescence architectural change, a change in stem bifurcations, a lack of a shoot meristem, reduced meristem cell differentiation, altered phyllotaxy, altered branching pattern, reduced apical dominance, reduced trichome density, ectopic trichome development, increased root growth, increased root hairs, altered seed development, altered cell proliferation/cell differentiation, premature senescence, delayed senescence, lethality, increased necrosis, an increase in seedling or plant size, decreased plant size, a change in leaf morphology, increased altered leaf development, increased leaf size and mass, glossy leaves, leaf cell expansion, change in seed morphology, altered seed coloration, increased seed size, decreased seed size, altered seed shape, change in leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid content, increased leaf insoluble sugars, decreased leaf fatty acid content, increased leaf anthocyanins, an alteration of leaf glucosinolate content, change in seed oil content, increase in seed fatty acid content, decrease in seed protein content, increase in seed protein content, decrease in seed oil content, alteration in seed prenyl lipid content, increase in seed sterols, upregulation of genes involved in secondary metabolism, increase in root anthocyanins, increase in plant anthocyanins, and alteration in light response or shade avoidance. The present sequence encodes an orthologue of a thalecress transcription factor isolated from Soybean.

SQ Sequence 974 BP; 294 A; 177 C; 195 G; 308 T; 0 U; 0 Other;

XX

Alignment Scores:
 Pred. No.: 1 AspGlyPhelystPArgLysTyrGlyLysLysValValValAspGly 20
 Score: 3.48e-26
 Percent Similarity: 90.74%
 Best Local Similarity: 83.33%
 Query Match: 12
 DB: 582 GATGGTACAGTGAGGAAGTGGCAGAAGTCGAGGCAATCTTACAG 523

XX

SQ Sequence 974 BP; 294 A; 177 C; 195 G; 308 T; 0 U; 0 Other;

XX

Alignment Scores:
 Pred. No.: 1 AspGlyPhelystPArgLysTyrGlyLysLysValValValAspGly 20
 Score: 247.00
 Percent Similarity: 90.74%
 Best Local Similarity: 82.89%
 Query Match: 12
 DB: 522 AACTACTAACATTCTAGTGGAGTCAGTGATAACATGAGGTGCAAC 463

RESULT 14

XX

Qy 21 AsnThrTyrLysCysSerSerGluGlyCysSerValLysLysValValAspGly 40
 Db 582 GATGGTACAGTGAGGAAGTGGCAGAAGTCGAGGCAATCTTACAG 523

XX

Qy 21 AsnThrTyrLysCysSerSerGluGlyCysSerValLysLysValValAspGly 40
 Db 522 AACTACTAACATTCTAGTGGAGTCAGTGATAACATGAGGTGCAAC 463

XX

Qy 41 AspAspAlaAlaLysValLeuThrThrTyrGluGlyValValHis 54
 Db 462 GATGACTACAGCTACGTGATAACATGAGGTGCAAC 421

RESULT 14

XX

ID AD062502 standard; DNA: 974 BP.
 XX

Qy 41 AspAspAlaAlaLysValLeuThrThrTyrGluGlyValValHis 54
 Db 462 GATGACTACAGCTACGTGATAACATGAGGTGCAAC 421

XX

Transcription factor G1274 orthologous sequence, SEQ ID 969.

XX

Plant; transcription factor; transgenic plant; abiotic stress tolerance; osmotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds. Glycine max.

OS

| | | | |
|-----|---|-------------------------------------|---|
| XX | WO2004031349-A2. | Qy | 1 AspGlyPhelystTParglystTyrGlyLysSerVallysAsnAsnIleasnlysArg 20 |
| PN | 15-APR-2004. | Db | 582 GATGGATACAGTGCGGGAGTACCCGAGAAGTCGTAGAGCTGAACTCAACTAAGG 523 |
| XX | 18-SEP-2003; 2003WO-US030292. | Qy | 21 AsnTyrTyrLysCysSerSerGluGlyCysSerVallysArgValGluArgAspGly 40 |
| PF | | Db | 522 AACTACTACAATGTTCAACTGGAGATCGATGTAAGGTGAAAGGTGATAAGGTGAC 463 |
| XX | 18-SEP-2002; 2002US-0434166P. | Qy | 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54 |
| PR | 17-DEC-2002; 2002US-0434166P. | Db | 462 GATGACTACAGCTACGTGATAACACATATGAAGGTGTGCAC 421. |
| PR | 24-APR-2003; 2003US-0465899P. | | |
| XX | (MEND-) MENDEL BIOTECHNOLOGY INC. | | |
| PI | Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL; | RESULT 15 | |
| PI | Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK; | ID ADI43067 standard; DNA: 1696 BP. | |
| XX | | XX | |
| DR | WPI; 2004-330163/30. | AC | ADI43067; |
| XX | | XX | |
| PT | New recombinant polynucleotide encoding transcription factor | DT | 22-APR-2004 (first entry) |
| PT | polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant. | XX | |
| XX | | DE | Plant transcription factor polynucleotide #1005. |
| PS | Claim 1; SEQ ID NO 969; 510pp; English. | XX | |
| XX | The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (AB061534-AB063778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to osmotic stress, increased tolerance to cold, increased germination in cold, increased tolerance to heat, increased germination in heat, increased tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to disease, including fungal disease and particularly Erysiphe, Fusarium and Botryotinia, increased tolerance to ACC, altered sugar sensing, increased resistance to glyphosate, increased sensitivity to ACC, reduced sensitivity to ABA, increased sensitivity to ACC, altered carbon/nitrogen sensing, early flowering, late flowering, altered flower structure, loss of flower dormancy, reduced fertility, altered shoot meristem development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced apical dominance, altered trichome density, altered trichome development, avoided trichome structure, altered root development, altered shade avoidance, altered seed development, altered seed ripening, altered seed germination, slow growth, fast growth, altered cell differentiation, altered cell proliferation, altered cell expansion, altered phase change, altered senescence, abnormal embryo development, altered programmed cell death, lethality when overexpressed, altered necrosis patterns, increased plant size, increased biomass, large seedlings, dwarfed plants, dark green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed coloration, altered seed size, altered seed shape, large seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seed prenyl content, altered leaf prenyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. | OS | Zea mays. |
| XX | | XX | |
| XX | | XX | |
| XX | | XX | US2004019927-A1. |
| XX | | PD | 29-JAN-2004. |
| XX | | PP | 25-FEB-2003; 2003US-00374780. |
| XX | | PR | 18-APR-2001; 2001US-00837944. |
| XX | | XX | |
| CC | (SHERMAN B. K. (RIEC.) RIECHMANN J. L. | PA | |
| CC | (JIAN/) JIANG C. | PA | |
| CC | (HEAR/) HEARD J. E. | PA | |
| CC | (HAAK/) HAAKE V. | PA | |
| CC | (CREELMAN R. A. (RATC.) RATCLIFFE O. | PA | |
| CC | (ADAM L. J. (REUB/) REUBER T. L. | PA | |
| CC | (KEDDIE J. (BROW/) BROWN P. B. | PA | |
| CC | (PILG/) PILGRIM M. L. | PA | |
| CC | (DUBB/) DUBBELL A. N. | PA | |
| CC | (PINN/) PINEDA O. | PA | |
| CC | (YUGG/) YU G. | PA | |
| XX | | XX | DR WPI; 2004-132245/13. |
| XX | | XX | |
| PI | Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V; | PT | New transgenic plant comprising a recombinant polynucleotide of any one |
| PI | Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, | PT | of more than 500 nucleotide sequences, useful in bioinformatic search |
| PI | Pineda O, Yu G; | PT | methods. |
| XX | | XX | |
| PS | Claim 1; SEQ ID NO 1530; 435pp; English. | XX | |
| DB: | | CC | The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully |
| XX | | CC | |
| SQ | Sequence 974 BP; 294 A; 177 C; 195 G; 308 T; 0 U; 0 Other; | | |

Alignment Scores:
 Pred. No.: 3.48e-26
 Score: 247.00
 Percent Similarity: 90.74%
 Best Local Similarity: 82.33%
 Query Match: 82.89%
 DB: 12
 XX

Length: 974
 Matches: 45
 Conservative: 4
 Mismatches: 5
 Indels: 0
 Gaps: 0

XX

US-10-666-642-194_COPY_111_164 (1-54) x ADO62502 (1-974)

defined in the specification or its complement. The method of the invention can be used to produce a plant having altered traits such as: enhanced tolerance to abiotic stress; glycophosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; early or late flowering; altered flower structure; change in stem bifurcations; altered branching pattern; reduced apical dominance; reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered trichome development; increase in trichome number; altered stem morphology; increased root growth; increased root hairs; altered seed development; altered cell proliferation or cell differentiation; rapid development; premature senescence; increased necrosis; increase in seedling or plant size; decreased plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant anthocyanins; or alteration in light response or shade avoidance. The transgenic plant, polynucleotides and polypeptides are useful in bioinformatic search methods. This sequence represents a plant transcription factor, and an orthologue of *Arabidopsis thaliana* transcription factors isolated in the invention, that can be used in the creation of a transgenic plant with altered traits.

XX Sequence 1696 BP; 433 A; 436 C; 407 G; 420 T; 0 U; 0 Other;

| Alignment Scores: | | | | | |
|------------------------|--------|---------------|------|--|--|
| Pred. No.: | 2e-25 | Length: | 1696 | | |
| Score: | 244.00 | Matches: | 43 | | |
| Percent Similarity: | 88.89% | Conservative: | 5 | | |
| Best Local Similarity: | 79.63% | Mismatches: | 6 | | |
| Query Match: | 81.88% | Indels: | 0 | | |
| DB: | 12 | Gaps: | 0 | | |

US-10-666-642-194_COPY_111_164 (1-54) × AD143067 (1-1696)

| Qy | 1 ASPGlyPheLysTrpArgLysTrpArgLysLysSerValIleAsnTleAsnLysArg 20 |
|----|--|
| Db | 394 GATGGATTCAAATGGGGAACTATGCCAAGGCTGTAAGTAGCCAAATCCAGG 453 |
| Qy | 21 AsnTyrrIlysCysSerSerGluGlyCyservalLysSarvalGluargaspGly 40 |
| Db | 454 AACTACTACCCCTGCTGAGGGCTGGCGGTGAAGAGCGGGTGAAGGGACCCC 513 |
| Qy | 41 AspAspAlaAlaAlaTyrValIleThrThrTyrGluglyvalHis 54 |
| Db | 514 GACGACCCCCCTAACCTCATCACACCCTAACCTCATCACGCCGTCAC 555 |

Search completed: August 26, 2005, 00:18:37
Job time : 397 secs

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